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OM nucleic - nucleic search, using sw model	<pre>March 31, 2004, 13:52:29 ; Search time 3483 Seconds (without alignments) 7167.840 Million cell updates/sec</pre>
- nucleic s	March
OM nucleic	Run on:

ļ	(Without Alignments) 7167.840 Million cell updates/sec
Title:	US-09-975-856-1
Perfect score:	576
Sequence:	1 ATGAACGGAGGCCTTATGACGAGTAACTCCCCTCG 576

		6940544
IDENTITY NUC Gapop 10.0 , Gapext 1.0	3470272 seqs, 21671516995 residues	Total number of hits satisfying chosen parameters:
Scoring table:	Searched:	Total number of

<pre>GenEmbl:* 1: gb_ba:* 2: gb_ntg:* 3: gb_in:*</pre>
Database :

GenEmbl:*	gp_ba:*	gb_htg:*	gp_in:*	ab om:	*: vo de	gb_pat:*	ab_th:*	gb_p1:*	gb_pr:*	gb ro:*	gb_sts:*	gb_sy:*	gb_un:*	gb_vi:*	em_ba:*	em_fun:*	em_hum:*	em_in:*	em_mu:*	em om:*	em or:*	em_ov:*	* · Tect mo
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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100.0%; Score 576; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;
Matches 576; Conservative 0; Mismatches 0; Indels C
                Length 576;
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Best Local Similarity 100.0%; Pred. No. 2.6e-164;
Matches 576; Conservative 0; Mismatches 0;
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Gure, A.O., Tureci, O., Sahin, U., Tsang, S.,
Pfreundschuh, M., Old, L.J. and Chen, Y.-T.
SSX family proteins
Patent: US 6329140-A 1 15-JAN-2002,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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    .576
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    /mol_type="unassigned DNA"

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AR182977.
AR182977.1 GI:20226184
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                                                                                                                    Length 576;
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                                                                                                                  100.0%; Score 576; DB 6; L. Larity 100.0%; Pred. No. 2.6e-164; Conservative 0; Mismatches 0;
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1 (bases 1 to 576)

Gure,A.O., Tureci,O., Sahin,U., Tsang,S.,

Pfreundschuh,M., Old,L.J. and Chen,Y.-T.

Isolated nucleic acid molecules encoding.
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/wol_type="unassigned DNA"
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Location/Qualifiers
1. .576
S 6287756-A 5 11-SEP-2001;
Location/Qualifiers
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Sequence 1 from patent US 6291658.
AR170503.1 GI:17908462
                                  1. .576
/organism="unknown"
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                                                                                                                                    Similarity
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 Patent:
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VERSION
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                       121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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LUDWIG INSTITUTE FOR CANCER RESEARCH
SLOAN-KETTERING CANCER CENTER (US);
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/db_xref="taxon:9606"
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organism="Homo
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/codon_start=1
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Location/Qualifiers
1..576
/organism="unknown"
/mol_type="genomic DNA"
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Tureci,O., Sahin,U., Pfreundschuh,M., Rammensee,H.G.
Stevanovic,S.
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Pred. No. 2.6e-164;
Mismatches 0; Indels
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Matches 576; Conservative 0;
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BD218420 SX gene, method of determining the occurrence of cancer in sample by determining the expression of peptides originating in the SSX gene and WY-ESO-1 gene and utilization thereof. BD218420 BD218420 I :33028190 JP 2002519013-A/5. Howo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   Topology: Linear;
Isolated nucleic acid molecules encoding SSX family members
and uses
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/organism='Unidentified'
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larity 100.0%; Pred. No. 2.6e-164;
Conservative 0; Mismatches 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Gure, N.C., Tureci, O., Sahin, U., Tsang, S., Scanlan, M.J., Knuth, A.
Pfreundschuh, J. old, L.J. and Chen, Y.T.
Isolated nucleic acid molecules encoding SSX family members and
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Isolated nucleic acid molecules encoding SSX family members and
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Daten: JP 200157408-A 1 25-DEC-2001;

LUDMIG INSTITUTE FOR CANCER RESEARCH, MEMORIAL SLOAN KETTERING
CANCER CENTER, CORNELL RESERCH FOUNDATION
OS Unidentified
N JP 2001527408-A/1
PD 25-DEC-2001
PP 25-DEC-2001
PP 25-FEB-1998 JP 1998548050
PR 05-MAY-1997 US 08/851138
PI ALI O GURE, OZLEM TURECI, UGUR SAHIN, SOLAM TSANG, MATTHEW J
                                                                                                                                                                                                                                                                                                                                                                                                                         TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGGAAGAAAA
                                                                                                                      AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAACTATGAGGTCATGACTAAA
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                                                     ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAAG
                                                                                  ATGAACGGAGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
                                                                                                                                                                                            AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
                                                                                                                                                                                                                                                             CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
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                                                                                                                                                                                                                                                                                                                                                              GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
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                   Indels
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red. No. 2.6e-164;
Mismatches 0;
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     Pred.
                     0;
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BD096872.1 GI:22642460
JP 2001527408-A/1.
unidentified
100.0%;
                     576; Conservative
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   Best Local Similarity
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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REFERENCE AUTHORS

BD096872

RESULT

JOURNAL

COMMENT

TITLE

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/db_xref="G1:2952023"
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sloriffhymkkrafberdikerybrasgpondokolicpponpstlektinktsgepkrg
khawthrlrerrkolivyyebisdpeeddde"
                                                                                                                                                                                             PRI 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="corresponds to the 5' PCR primer that was used to isolate this gene and is identical to SSX2, GenBank Accession Number X86175; therefore, the SSX4 gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gure, A.O., Tureci, O., Sahin, U., Tsang, S., Scanlan, M.J., Jager, E., Kuth, A., Pfreundschuh, M., Old, L.J. and Chen, Y.T. SSX: a multigene family with several members transcribed in normal testis and human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="SSX4"
note="putative translation product; Kruppel-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 576)
Gure, A.O., Tureci,O., Sahin,U., Tsang,S., Scanlan,M., Knuth,A.
Pfreundschuh,M., Old,L.J. and Chen,Y.-T.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 576)
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                                                                                                                                                                                             linear
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        576
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Submitted (05-FB1997) Pathology C-320,
York Ave., New York City, NY 10021, USA
Location/Qualifiers
                                                                                                                                                                                           576 bp mRNA mRNA complete
                                    AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
        541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Int. J. Cancer 72 (6), 965-971 (1997) 98021352
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/product="SSX4"
/protein_id="AAC05820.1"
/db_xref="GI:2952023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
1. .576
                                                                                                                                                                                                   Homo sapiens SSX4 (SSX4)
U90841
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DY 2002519013-A/5

PD 02-JUL-2005

PP 25-JUN-1999 UP 09/105839

PR 26-JUN-1998 US 09/105839

PI OZLEM TURECI, VGUR SAHIN, MICHAREL PFREUNDSCHUH, GEORG RAMMENSEE, PI STEFAN STEVANOVIC, RAO TSENG CHEN, ALI GURE, LLOYD J OLD PC CILNIS/09, A61K38/00, C07H21/04, C12N5/10, C12P21/04, C12Q1/68, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sample by determining the expression of peptides originating in the SSX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAAACTATGAGGTCATGACTAAA 180
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                              Stevanovic, S.,
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                   Tureci.(). Sahin,U., Pfreundschuh,M., Rammensee,G., Steva,Chen,Y.T., Gure,A. and Old,L.J.
SSX gene, method of determining the occurrence of cancer by determining the expression of peptides originating in Patent: JP 2002519013-A 5 02-JUL-2002;
LUDDWIG INSTITUTE FOR CANCER RESEARCH
PN JP 2002519013-A/5
PN JP 2002519013-A/5
PN JC-JUL-2002
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13. (bases 1 to 1250)

14. (bases 1 to 1250)

15. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

15. Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

16. Altschul, S.F., Zeeberg, B., Buttow, K.H., Schaefer, C.F., Bath, N.K.,

17. Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

18. Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

18. Scarse, M.B., Bonaldo, M.F., Casavanth, T.L.,

18. Schaefer, M.B., Bonaldo, M.F., Casavanth, T.L.,

18. Schaefer, M.B., Bonaldo, M.F., Casavanth, T.L.,

18. Schaefer, M.B., Bonaldo, M.F., Toshiyuki, S.

18. Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

18. Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

18. Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

18. Worley, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

18. Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

18. Blakesley, R.W., Touchman, J.W., Green, E.D.,

18. Dickson, M.C., Rodriguez, A.C., Grimocod, J., Schmutz, J., Myers, R.M.,

18. Blakesley, R.W., Touchman, J., Schmutz, J., Myers, R.M.,

18. Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

18. Generation and initial analysis of more than 15,000 full-length

18. Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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                                                                                                                                                          TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGCAGGAAGAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                   421 CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAAGGGGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATTC 540
CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
                                                      GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAAACGTCCTCAGATGACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens synovial sarcoma, X breakpoint 4, transcript variant 1, mRNA (cDNA clone MGC:12411 IMAGE:3961688), complete cds.
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Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u> AAACATGCCTGGACCCACAGACTGCGTGAGAAAAGCAGCTGGTGTTTTATGAAGAGATC</u>
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cDNA Library Preparation: CLONTBCH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
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KHAWTHRIRRRKQLVYVEEISDPEEDDE"
                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: m Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28559011.
Location/Qualifiers
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                                                                                                                                                                                                                        Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="gynovial sarcoma, X breakpoint 4, isoform a"
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/note="KRAB; Region: krueppel associated box"
/db_xref="CDD:smart00349"
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/tissue type="Bladder, carcinoma"
/clone_lib="NHH_MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 574.4; DB 9;
Pred. No. 8.8e-164;
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Db 452 AATGATTCGGAGGAAGTGCCAGAAGTTAACAAATGATGGGAAAGGGTGTGC 511 Qy 421 CCCCGGGAAATCCAAGTGCTTGAGAAGATTAACAAGACATTGACGAAGAGGGG 480		ACCACGCCTT ACCACGCCTT CONTROL ACCACGCCTC ACCACCACCT ACCACCACCT ACCACCACCC ACCACCACCCC ACCACCACCCCC ACCACC
359 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGGAAGAA 418 361 AATGGTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAATGATGGCAAACAGCTGTGC 420 419 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAATGATGGGAAAACGTGTGC 478 421 CCCCCGGGAAATCCAACTACCTTGGAGATTAACAAGACATCTGGAACCCAAAAGGGGG 480 419 CCCCCGGGGAAATCCAAGTACCTTGGAGAATTAACAAGACACCCAAAAGGGGG 538 479 CCCCGGGGAAATCCAAGTACCTTGGAGAATCAAGAGACCCAAAAGGGGG 538 481 AAACATGCCTGGACCAACAGACTGGTGAGAAACAGCTGGTGGTTTATGAAAAGAGGGG 538 539 AAACATGCCTGGACCCACAGACTGGTGAGAAAACAGCTGTTATGAAAAAAAC 598	QY 541 AGCGACCCTGAGGAAGATGACGACTCCCTCG 576	Guery Match Query Match Query Match Query Match Best Local Similarity 91.3*; Pred. No. 4.5e-140; Matches 526; Conservative 0; Mismatches 49; Indels 0; Gaps 0; 1 ATGAACGAGACGACCTTTGCAAGGAGACCCCAACTATACAATATCAAGAAG 60 1 TACGAAAGCCTTTGCAAGGAGACCCCACGATGATGATCAATATCAAGAAGG 151 61 TTACGAAAGGCCTTTGCAAGGAGACCCACGGATGATGATCAATATCAAGAAGG 151 152 ATGAACGGAGACGACGTTTGCAAATACTTCTTAAGAAAGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules which encode renal cancer specific antigens, and uses thereof
Patent: US 5798264-A 2 25-AUG-1998;
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                                                                 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                    332 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         632 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC
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Sequence 2 from patent US 5798264.
AR025465
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Pfreundschuh, M.
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Unclassified.
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KEYWORDS
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RLQFISPKIMPKKPAEGNDSEEVPPASGPQNDGKELCPPGKPTTSEKIHERSGPKRG
EHAWTHRRERRQLYYEEISDPEEDDE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooper, C.S.
Direct Submission
Submitted (10-AER-1995) C.S. Cooper, Institute of Cancer Research, Haddow Laboratories, Cotswold Road, Sutton, Surrey SM2 5NG, UK
Location/Qualifiers
       540
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                                                                                                                                                                                                                                                                                                                                                                    Crew, A.J., Clark, J., Fisher, C., Gill, S., Grimer, R., Chand, A., Shipley, J., Gusterson, B.A. and Cooper, C.S. Fusion of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma EMBO J. 14 (10), 2333-2340 (1995)
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             572 GAACAIGCCIGGACCCACAGACIGCGIGAGAAAACAGCIGGIGAITIAIGAAGAGAATC
     481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAATC
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/gene="SSX2"
/note="Kruppel aaociated box homology"
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llarity 91.5%; Pred. No. 4.6e-140;
Conservative 0; Mismatches 49;
                                                                       575
                                                                                                      632 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 666
                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                 SSX1 gene; SSX2 gene; synovial sarcoma.
Homo sapiens (human)
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X86175.1 GI:829113
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Db 459 AATGATTCGGAGGAAGCATCTGGCCCACAAAATGATGGGAAAGGGGG 518 Qy 421 CCCCCGGGAAATCCAAGTGCTTGGACAGATTAACAAGACATCTGGACCCAAAAGGGGG 480	RESULT 15 ARI17874 LOCUS LOCUS DEFINITION Sequence 2 from patent US 6140464. ACCESSION ARI17874 VERSION WERSION KEYWORDS ONGANISM Unclassified. TITLE AUTHORS Freundschub, M. and Rammensee, HG. TITLE JOURNAL Patent: US 6140464-A 2 31-OCT-2000; FRATURES LOCATION/QUalifiers SOURCE JOURNAL Patent: US 6140464-A 2 31-OCT-2000; FRATURES LOCATION/QUalifiers JOURNAL Patent: US 6140464-A 2 31-OCT-2000; FRATURES JOURNAL Patent: US 6140464-A 2 31-OCT-2000; FRATURES JOURNAL PATENT: LOCATION/QUALIFIERS JOURNAL PATENT: US 6140464-A 2 31-OCT-2000; FRATURES JOURNAL PATENT: US 6140464-A 2 31-OCT-2000; JOURNAL PATENT:	Design	Db 159 ArccadadgeCtricGalgatatricCchainactrictcriaggadagadaddig 218 Oy 121 AdatecteggagaaaategtetatatgeGtatatgageCtatagageTeataga 180 Db 219 AdageCtreggagaaaatettetatgeGtatagagagaaagtatgaggeTatagagagaaaa 278 Oy 181 CTAGGTTTCAAGGTCACCTCCCACCTTTCATGGTAGAAAGGGCTGCAGACTTCCAC 240 Db 279 CTAGGTTTCAAGGTCACCTCCCACCTTTCATGGTAGAAACGGCCTGCAGACTTCCAC 240 Db 279 CTAGGTTTCAAGGCCACCTCCCACCTTTCATGTGTATAAACGGGCCGAAGACTTCCAC 338	Qy 241 GGGAATGATTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300 Db 339 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTTGAACGTCGATGACT 398 Qy 301 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGAACCCAAGAAGCCAGCAGGAAGAA 360 Db 399 TTCGGCAGGCTCCAGGGAATCTCCCCGAAGATCATGCCCAAGAAGCCAGCAGGAAGAA 458	QY 361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAATGATGGGAAACAGCTGTGC 420 Db 459 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGAAAAGAGTGC 518 QY 421 CCCCCGGGAAAATCCAAGTACCTTGGAGAAGTTAACAACAACACACCAAAAGGGG 480 Db 519 CCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGAACTTGGACCCAAAAGGGG 578 QY 481 AAACATGCCTGGAGAACTCTCTGAGAAAGCAGCAGTGATGATAATGAAGAGTC 540	
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579 GAACATGCCTGGACCCACAGACTGCGTGAGAGAAACAGCTGGTGATTTATGAAGAGATC 638

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1 ATGAACGGAGGACGCCTT.....ATGACGAGTAACTCCCCTCG US-09-975-856-1 Perfect score: Title:

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3373863 seqs, 2124099041 residues Gapop 10.0 , Gapext 1.0 Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description		Abk84472 Human cDN	Abg83858 Human SSX	Adc09598 SSX-4 cDN	Aav70060 Human SSX	Aat11780 Human X-c	Abs73282 DNA encod	Aad54033 Human col	Abg83844 Human SSX	_	Add25523 Binding d	Aat47748 Melanoma	Aav04267 Melanoma	Abl64122 Breast ca	Abl63730 Breast ca	Aas80402 DNA encod	Aas80399 DNA encod	Aav70061 Human SSX	Aat11779 Human X-c	Aat11781 Human SYT	Aat11782 Human SYT	Aas80401 DNA encod	Aas80404 DNA encod	Abs73281 DNA encod
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ALIGNMENTS

Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; andlt respiratory distress syndrome; inflammatory bowel disease; Crohm's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy. Human cDNA differentially expressed in granulocytic cells #1043. BP. ABK84472 standard; cDNA; 576 (first entry) 14-AUG-2002

03-OCT-2001; 2001WO-US030821. 03-OCT-2000; 2000US-0237189P. WO200228999-A2. Homo sapiens 11-APR-2002.

(GENE-) GENE LOGIC INC.

Vockley J; Yamaga S, Weissman SM, Beazer-Barclay Y,

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

claim 1; SEQ ID NO 1043; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis a sgiven in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are

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capable of adulating Mes. So not contain an agent that are are the agent and are are the agent capable of adulating GCA or an inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (MA) an inflammation (especially chronic) in a profile; (3) detecting (MA) an inflammation (especially chronic) in a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene (s) from Gs in the tissue. MI consistent that modulates the expression of gene (s) from Gs in the tissue. MI consistent in a utissue, M4 is useful for detecting an agent capable of modulating GA preferably in an inflammation in a tissue, an allergic response in a subject, or exposure of a subject to a pathogen or sterile inflammatory disease (e.g. profiles experies); the an allergic response in a subject, or exposure of a subject to a pathogen or sterile inflammatory disease (e.g. profiles experies); theumatoid arthritis, glomerulonephitis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, renal reperfusion injury, renal reperfusion injury, renal reperfusion injury, and response in a contacting a crepitatory distares, spridtent inflammatory disease, contacting a crepitation in a contacting an inflammatory disease, contacting a crepitation injury, renal reperfusion injury, and in the contacting an inflammatory disease, contacting a contacting a contacting an inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, ulcerative colitis, periodoncal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent not form part of the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
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The present invention describes an isolated epitope (1) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (1). (1) has cytostatic activity. VC is useful for treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic composition. VC is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic composition, by administering VC to an HiA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (1) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis limiting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PCR). ABQ33843 to ABQ33858 and ABP74128 to ABP747;3 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                       epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel epitopes useful as vaccines, comprises peptides or nucleic acioencoding the peptides, that are useful epitopes of target-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 576; 9.3e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 576 BP; 187 A; 127 C; 150 G; 112 T; 0 U; 0 Other;
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                              541 Acceaccercaccaacarcaccacracecececce 576
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100.0%; Pred. No. 9.3
ive 0; Mismatches
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                                                                                                                                                                                                                     Human SSX-4 encoding cDNA SEQ ID NO:599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 185; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CTLI-) CTL IMMUNOTHERAPIES CORP
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07-NOV-2001; 2001US-0337017P.
07-MAR-2002; 2002US-0363210P.
                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2002; 2002WO-US011101.
                                                                                                                  ABQ83858 standard; cDNA; 576
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Conservative
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                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Matches 576;
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epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy. blochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC -peptide complexes of the invention are useful for determining specific T call frequency. This method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for diagnosing a disease. The current sequence represents an epitope of the
                                                                                                                                                                                                                                                                                                                                                      ATGAACGGAGACGCCTTTGCAAGGACCCCAGGGATGATGATGCTCAAATATCAGAGAAG 118
                                                                                                                                                                                                                                                                                                                                                                                                      TTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGAAGAGAGTGGGAAAAGATG 120
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                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                           100.0%; Score 576; DB 9; Length 1250; 100.0%; Pred. No. 1.4e-171; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                            Sequence 1250 BP; 373 A; 302 C; 278 G; 297 T; 0 U; 0 Other;
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invention with high affinity for MHC class I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epitope having high affinity for major histocompatibility complex class useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.
                                                                                         The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an
                                  AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAAACTATGAGGTCATGACTAAA
AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
                                                                    CTAGGITTCAAGGICACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
                                                                                                                                                                                                       TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAAGAA
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major histocompatibility complex class I; MHC class I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG 576
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07-MAR-2002;
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us-09-975-856-1.rng

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481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; SSX2 gene; synovial sarcoma; X-chromosome; breakpoint-2; ornithine-delta-aminotransferase; OATL2 gene; Xpl1.2; SSX1 gene; translocation; chromosome-18; 18q11.2; SYT gene; gene fusion; SYT-SSX2; fusion protein; primer; PCR; polymerase chain reaction; Smal; LpsI; probe; antibody; monoclonal antibody; humanised antibody; hybridisation; antisense; antitumour; recombinant vaccine; vaccinia virus; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing synovial sarcoma by detection of e.g. SYT and SSX1 sequences, based on X18 trans-location - by amplification of trans-location sequences or detection of the encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the SSX2 gene (synovial sarcoma X-chromosome breakpoint-2). The gene is at the location of a breakpoint at Xp11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= f
/note= "3'-Region present in SYT-SSX2 fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/note= "Breakpoint for SYT translocation"
                                                                                                AGCGACCTGAGGAAGATGACGAGTAACTCCCCTCG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '*tag= g
'note= "Binds primer AAT11784"
                                                     AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/codon= seq:TTC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b /codon= seq:AAG, misc_difference 257. .259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon= seq:GAG,
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/codon= seq:CGT,
                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; diagnosis; therapy; ss.
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                                                                                                                                                                                                                                     AAT11780 standard; cDNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                       Human X-chromosome SSX2 cDNA
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P-PSDB; AAR90677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                             New SSX gene family members - useful for assaying for cancer cells.
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                                                                                                                                                                                                                                                                                              Knuth
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Pred. No. 3e-171;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                           O, Sahin U, Tsang
Old LJ, Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 12; 19pp; English
                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
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Pfreundschuh M,
                      W09850528-A1
                                                                                                                            25-FEB-1998;
                                                                                                                                                                                  05-MAY-1997;
                                                                      12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCAAAAGGCCTTCGATGATAGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAACGGAGACGACGTTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAGGITTCAAGGCCACCCTCCCACCTTTCATGTGTAATAAACGGGCCGAAGACTTCCAG 331
                the translocation t(X;18) (p11.2;q11.2) found in human synovial sarcomas, involving joining of the SYT gene (AAT11778) on chromosome-18 at 18q11.2 to SSX2. The gene fusion is then transcribed to produce an SYT-SSX2 (AAT11781) fusion transcript and translated into a fusion protein. SSX2 may be distinguished from related sequence SSX1 (AAT11779) by digestion with Smal and Lept. Primer AAT11784 has been used in polymerase chain reaction amplification of SSX2 sequences. Detection of the gene or its product in an abnormal location or as a fusion may be used in diagnosis
                                                                                                                                                                            of synovial sarcoma, using primers, probes, humanised antibodies, monoclonal antibodies, etc. Antisense oligonucleotides and antibodies also be used therapeutically, and antitumour recombinant vaccines may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTAGGITICAAGGICACCCICCCACCTITCAIGCGTAGIAAACGGGCIGCAGACITCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCCAAAAATGATGGGAAAGAGCTGTGC
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Pred. No. 1.5e-146;
within an ornithine-delta-aminotransferase OATL2
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91.5%;
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Matches 526; Conserv
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92 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG 151 cracerricaacccacccrcccaccrrrcarcrararaaaccccaacacrrcaac 331 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90. or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Bwing's sarcoma, melanoma, libosarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This represents the DNA sequence of a chromosome aberration HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; 1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG 152 Arccaragecerregargararreceaarracriceraageagaagagagaaaagare AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAACTATGAGGTCATGACTAAA AAAGCCTCGGAGAAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC Gaps ; 0 Length 766; rhabdomyosarcoma; synovial sarcoma; viral infection; gene; 766 BP; 229 A; 181 C; 200 G; 156 T; 0 U; 0 Other; Indels 49; DB 6; Query Match 86.2%; Score 496.6; DB 6; Best Local Similarity 91.5%; Pred. No. 1.5e-146; Matches 526; Conservative 0; Mismatches 49; Disclosure; Page 236; 389pp; English (CONF-) CONFORMA THERAPEUTICS 01-MAR-2001; 2001US-0272751P. 01-MAR-2002; 2002WO-US006518 Burrows FJ; WPI; 2002-698710/75. P-PSDB; ABG95081 WO200269900-A2 Homo sapiens 12-SEP-2002 ĽĊ, 212 Sequence 61 121 181 Fritz à g ð qq à g à q Chromosome aberration, oncogenic fusion protein; cancer, proliferative disease; cellular protein isoform; heat shock protein 90;

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120 211 180 271 240

DNA encoding human translocation (X; 18) (p11.2; q11.2) protein

(first entry)

04-DEC-2002

ABS73282 standard; DNA; 766

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Length 766;

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vaccine; immunotherapeutic; cytostatic; immunogenicity;
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                                                                                                 Arccaaaaggccrrcgargararricccaaaracrrcrcraaggaagagigggaaaagard
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                                                                                                                                            Score 496.6; DB 7;
Pred. No. 1.5e-146;
0; Mismatches 49;
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2001US-0337017P.
2002US-0363210P.
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86.2%;
91.5%;
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07-NOV-2001;
07-MAR-2002;
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   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAAACGTCCTCAGATGACT 300
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                                    GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
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                                                                                                 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                               <u> AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGAAGGAAAAGAGCTGTGC</u>
                                                                                                                                                                                                                       CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCCAAAAGGGGG
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The present invention describes an isolated epitope (I) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (I). (I) has cytostatic activity. VC is useful for reating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunotherapeutic composition. VC is also useful for evaluating immunotenicity of a vaccine or immunotherapeutic composition, by administering VC to an HLA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, climiting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to ABP74131 represent sequences used in the exemplification of the present
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                                                                                  Novel epitopes useful as vaccines, comprises peptides or nucleic acid encoding the peptides, that are useful epitopes of target-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.2%; Score 496.6; DB 7; Best Local Similarity 91.5%; Pred. No. 1.5e-146; Matches 526; Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              999
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                                                                                                                                                                         Claim 1; Page 148; 352pp; English.
                  2003-067518/06,
                                          P-PSDB; ABP74130
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Epitope having high affinity for major histocompatibility complex class I useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated epitope polypeptide that has high effinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemcherapy or biochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC repeptide complexes of the invention are useful for determining specific T cell frequency. This method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for disease. The current sequence represents an epitope of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
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                                                                                                                                           Epitope; immunological; vaccine;
major histocompatibility complex class I; MHC class I; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 766;
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91.5%; Pred. No. 1.5e-146;
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ADC09570 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diamond DC,
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Best Local Similarity
                                                                                                                                                                                immunisation; ss.
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0
                 Length 766;
                                                               Indels
              Score 496.6; DB 9;
Pred. No. 1.5e-146;
0; Mismatches 49;
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96US-00644116.
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                 Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
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10-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                  481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTTATGAAGAGTC 540
                                                                                                                                      TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGCAGAAGAA 360
                                                                                                                                                                                                                             AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                         AATGATTCGGAĞGAAGTGCCAĞAAĞCATCTĞGCCCACAAAATGATĞĞĞAAAGAĞCTĞTĞC 511
                                                                                                                                                                                                                                                                                                                          CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
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CTAGGTTTCAAGGCCACCCTCCCACCTTTCATGTAATAAACGGGCCGAAGACTTCCAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                           GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                       GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCTCAGATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding domain-immunoglobulin fusion protein-associated DNA #46
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2002US-00053530.
2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-801317/75.
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03-JUN-2002;
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molecules

Novel method of serological fishing - allows isolation of molecule antigens) associated with pathological conditions, e.g. Hodgkin's disease, cancer or auto:immune disease. Claim 31; Page 29; 44pp; English WPI; 1997-051896/05

designated HOM-MEL 40. It was isolated using a novel method in which a designated HOM-MEL 40. It was isolated using a novel method in which a cDNA library prepd. from malignant melanoma and expressed in B. coli colls. Lysates of the host cells and with sera that had been treated to remove interfering binding partners. This involved contacting the sample with lysates of untransfected host cells and with host cells transformed with the same vector (phage lambda) used to make the CDNA library. The method, termed serological fishing, can be used to detect antigens in human tissues, esp. tumour cells, which are useful in the moliganosis of diseases and/or for immunotherapy and gene therapy of infectious, autoimmune and malignant diseases (see also AAA-4747-49). HOM-MEL 40 is expressed in 50% of melanomas, 20% of prostate cancers, 20% of gastric cancers, 20% of colorectal cancers, 12% of lung cancers and calls present a nonomer (see also AAW-09449- 52) derived from HOM-MEL, suggesting that HOM-MEL 40-specific vaccines, useful in inducing T lymphocytes, are possible

Seguence 931 BP; 274 A; 207 C; 231 G; 219 T; 0 U; 0 Other;

360 458 578 638 420 518 480 398 159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG 218 219 AAAGCCTCGGAGAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA 278 240 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGATGCAAAATATCAGAGAAG AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC TTCGGCAGCCTCCAGAGAATCTTCCCGGAAGATCATGCCCAAGAAGCCAGCAGGAGGAAGAA Tregeragerreraggaatereecegaagareargeeceaagaageeaggagggaagga AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAACAGCTGTGC AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAAGAGCTGTGC CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG cecededadadecraecreererendadadarreacadadareredadeceadadede GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAATC Gaps . 0 86.2%; Score 496.6; DB 2; Length 931; .larity 91.5%; Pred. No. 1.6e-146; Conservative 0; Mismatches 49; Indels 0 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575 Local Similarity les 526; Conser 519 279 301 399 361 459 421 481 541 241 339 121 181 Query Match Matches qq ð ద ð dd ò 유 g ò g δ q à g δ a à ð

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CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240

121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA <u> aaagcercogaagaaarrettetargtetatatgaagaaagaaagrargaggetargactaaaa</u>

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639 Agcgacccrgaggagaagargacgagraacrcccrc

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Clone HOM-MEL-40 was isolated from a human malignant melanoma oDNA clonery using a method, designated serological fishing, designed to identify immunoreactive markers of disease. In this method, cells characteristic of a disease are used to prepare a cDNA library for transformation of eukaryotic or prokaryotic cells, and the cells grown to express proteins. Patient serum is incubated with the cells used to prepare the library, but not transfected, to remove any components of the cells carrying the empty vector. The twice-stripped sample is similarly treated incubated with lysate of the library cells, so that specific components in the sample may bind to the expression protein. Proteins that form the sample may bind to the expression protein. Proteins that form melanoma, but not healthy tissues. The deduced amino acid sequence melanoma associated antigen is strongly expressed in melanoma, but not healthy tissues. The deduced amino acid sequence includes 1 tumour-associated peptides (see AAW41587-89) that bind to HIA-marker (see AAV04262) of Hodgkin's disease Nucleic acid and derived protein are markers for Hodgkin's disease - used in identifying immuno:reactive markers of disease. 1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGTCCAAATATCAGAGAAG 99 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG 159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGGTGGGAAAAAGATG Gaps marker; antigen; diagnosis; serological fishing; human; 0 Length 931; Sequence 931 BP; 274 A; 207 C; 231 G; 219 T; 0 U; 0 Other; Indels 86.2%; Score 496.6; DB 2; llarity 91.5%; Pred. No. 1.6e-146; Conservative 0; Mismatches 49; Example 7; Page 30-31; 47pp; English Melanoma antigen clone HOM-MEL-40. .. AAV04267 standard; cDNA; 931 BP (LUDW-) LUDWIG INST CANCER RES. 96US-00668128. 97WO-US010926. (first entry) WPI; 1998-063074/06. Best Local Similarity Matches 526; Conserv Pfreundschuh M; HOM-MEL-40; ss. WO9748721-A1. Homo sapiens. 23-JUN-1997; 21-JUN-1996; 22-JUN-1998 24-DEC-1997. Melanoma; Query Match AAV04267; AAV04267 qq qq ò à

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AAAGCCTCGGAGAAATCTTCTATGTGTATATGAGAGAAGTATGAGGCTATGACTAAA 278
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                                     GGGAATGATTTTGGTAACGATCGAAACCACGGAATCAGGTTGAACGTCCTCAGATGACT 300
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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25-SEP-2000; 2000US-0234923P.
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ne present in the method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in coprastion of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL66664 comprises a sequence (S) selected from 8447 sequences (given in ABL66664 comprises a sequence (S) selected from 8447 sequences (given in ABL66664 comprises indicative of anti-neoplastic activity. (I) has ofvostatic cartivity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is confirmed the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, appillary carcinoma and Wilm's cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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86.2%; Score 496.6; DB 6;
Best Local Similarity 91.5%; Pred. No. 1.9e-146;
Matches 526; Conservative 0; Mismatches 49;
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2000US-0236034P.

2000US-0236109P.

2000US-023641DP.

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2000US-0237278P.
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2000US-0237694P.
2000US-0237604P.
2000US-0237606P.
2000US-0237608P.
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Weaver Z;
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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent comprises of the for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in air least 95% identical to (S), where a change in comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is anti-neoplastic agent. M1 can be used in the treatment of cancer such the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such the convertient of the agent. M2 cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarionema, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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Pred. No. 1.9e-146;
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29-SEP-2000; 2000US-0236842P.
29-SEP-2000; 2000US-0236842P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237298P.
03-OCT-2000; 2000US-0237298P.
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01-NOV-2000; 2000US-024867P.
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Local Similarity 91.5%;
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Weaver Z;
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      GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                   339 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
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                                                                     TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAGGAAGAA
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18-SEP-2000; 2000US-023313P.
18-SEP-2000; 2000US-023313P.
20-SEP-2000; 2000US-023403P.
20-SEP-2000; 2000US-023403P.
20-SEP-2000; 2000US-023403P.
22-SEP-2000; 2000US-0234567P.
22-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234924P.
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                                                                              AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAAACAGCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #16206.
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P-PSDB; ABG16215.
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polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                  09
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                                                                                                                                                                                                                                        Sequence 921 BP; 267 A; 205 C; 233 G; 216 T; 0 U; 0 Other;
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84.6%; Score 487.2; DB 5;
Best Local Similarity 91.3%; Pred. No. 1.6e-143;
Matches 528; Conservative 0; Mismatches 48;
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Job time
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March 31, 2004, 15:19:29 ; Search time 97 Seconds
   (without alignments)
   3295.378 Million cell updates/sec
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1 ATGAACGGAGACGCCTT.....ATGACGAGTAACTCCCCTCG 576
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11. /ogn2_6/ptodata2/ina/5A_COMB.seq:*
12. /ogn2_6/ptodata2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /ogn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata2/ina/PCTUG COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUG COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                             682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli		Sequence 9992, Ap	Sequence 115, App	Sequence 3458, Ap	Sequence 5, Appli	Sequence 14, Appl	Sequence 147, App	٠,	Sequence 1092, Ap	Sequence 257, App	Sequence 3, Appli	Sequence 5, Appli	Sequence 5, Appli	Seguence 2813, Ap	Sequence 15639, A	Seguence 3471, Ap	Sequence 3333, Ap
US-09-833-039A-1	US-08-232-463-14	US-09-621-976-9992	US-09-976-594-115	US-09-621-976-3458	US-09-294-531B-5	US-08-179-557-14	US-09-620-312D-147	US-09-976-594-557	US-09-621-976-1092	US-09-641-638-257	US-09-881-578A-3	US-08-692-787-5	US-09-097-199-5	US-09-621-976-2813	US-09-621-976-15639	US-09-489-039A-3471	US-09-489-039A-3333
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181 CIAGGITICAAGGICACCCICCCACCIIICAIGCGIAAACGGIGGCGIAGGACTICCACACACACACACACACACACACACACACACACAC	121 AAATCCTCGGAGAAAATGGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 121 AAATCCTCGGAGAAAATGGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 181 CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 181 CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 181 CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC	RESULT 1 US-09-105-839D-5 Patent No. 6287756 GENERAL INFORMATION: APPLICANT: Tureci, Ozlem APPLICANT: Chen, Yao-Tseng APPLICANT: Old, Lloyd J APPLICANT: Sf CURRENT FILING DATE: 1990-06-26 PRIOR FILING DATE: 1997-05-05 NUMBER OF SEQ ID NOS: 72 IENCTH: Sf
121 AAATCCTCGGAGAAAATGGTCTTATGTATATGAAGCTAAACTATGAGGTCATGACTAAA 181 CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGGGGTAAAACGGGCTGCAGACTTCCAC 181 CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAAAACGGGCTGCAGACTTCCAC	121 AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAAACTATGAGGTCATGACTAAA	Query Match Best Local Similarity 100.0%; Pred. No. 1.7e-184; Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAACGGGGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG 1 ATGAACGGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG 1 ATGAACGGACGACGCCTTTGCAAGGAGACCCCAGGGATGATGCTCAAATATCAGAAAGA 61 TTACGAAAGGCCTTCGATGATTGCCAAATACTTCTTAAGAAGAGTGGGAAAAGATG 61 TTACGAAAGGCCTTCGATGTGTATTGCCAAATACTTCTTAAGAAGAGTGGGAAAAGATG 61 TTACGAAAGGCCTTCGATGTGTATTTGCCAAATACTTCTTAAGAAGAGTGGGAAAAGATG 61 TACGAAAGGCCTTCGATGTGTATTTGAAGCTTAAAGAAGATGGGAAAAGATG 62 AAATCCTCGGAGAAAATCGTCTATGTGTATTATGAAGCTAAAAGATGACTAAAA 63 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAAGATGACTAAAA 64 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAGAGTCATGACTAAA 65 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAAGTCAAAATTCGACTAAAATCGAAAATTCGAAAATTCGAAAAATCGAAAAATTCGAAAAATCGAAAAATTCGAAAAATTCGAAAAAACAAAAAACAAAAAAAA	1 ATGAACGGGACGACGTTTGCAAGAGACCCAGGGATGATGCTCAAATATCAGAGAAG	

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APPLICANT: Gure, Ali O.; Tureci, Ozlem, Sahin, Ugur; Tsang, Solam, APPLICANT: Scanlan, Matthew J.; Knuth Alexander; Pfreundschuh, Michael; Old, APPLICANT: Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX
TITLE OF INVENTION: Family
TITLE OF INVENTION: Family
TITLE OF INVENTION: Members And Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
STREET: 666 Fifth Avenue
CITY: New York City
                                                                                                                                                                                                                 241 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
                                                                                                                                                                             GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                             AAATCCTCGGAGAAAATCGTCTATGTGTATAAGCTAAACTATGAGGTCATGACTAAA 180
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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APPLICATION NUMBER: US/09/796,780
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/851,138
FILING DATE: 5-May-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09796780 ; Patent No. 6339140
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TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 1:
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OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gure, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: N
STATE:
      121
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Patent No. 6291658
Patent No. 6291658
Patent No. 6291658
Patent No. 6291658
Papticant: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Garalan, Matthew J.; Knuth Alexander; Pfreundschuh, Michael; Old, APPLICANT: Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX Family
TITLE OF INVENTION: Members And Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                   CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCGAAAAGGGGGG 480
                                                                                                                                                                                                                                            AAACATGCCTGGACCCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAATC 540
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AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAAAAGCTGTGC 420
                                                                                                          AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
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100.0%; Pred. No. 1.7e-184;
ive 0; Mismatches 0;
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CITY: New York City
STATE: New York
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REGISTRATION NUMBER: 30,946
REFERNICE/DOCKET NUMBER: LUD 5480
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 318-3168
TELEPHONE: (212) 752-5968
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,138C
FILING DATE: 5-May-1997
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS
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Best Local Similarity 100.
Matches 576; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-851-138C-1
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US-08-851-138C-1
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APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
TITLE SPENCH: Sahin, Ugur
TITLE OF INVENTION: Tureca Associated Peptide and Uses Thereof
TITLE OF INVENTION: Tureca Associated Peptide and Uses Thereof
TITLE OF INVENTION: Tureca Associated Peptide and Uses Thereof
CURRENT FILING DATE: 1099/83,039A
CURRENT FILING DATE: 1099-06-25
PRIOR APPLICATION NUMBER: US 09/44,040
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR PRILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PRILING DATE: 1998-06-26
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Pred. No. 1.7e-184;
0; Mismatches 0;
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; GENERAL INFORMATION:
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ilarity 100.08;
Conservative 0;
                             Homo sapiens
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Best Local Similarity
Matches 576; Conserv
    ; TYPE: DNA
; ORGANISM: Hom
US-09-344-040C-5
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APPLICANT: Tureci, Ozlem
APPLICANT: Bahin, Ugur
APPLICANT: Bahin, Ugur
APPLICANT: Breanese, Hans Georg
APPLICANT: Remensee, Hans Georg
APPLICANT: Repression of an SSX Gene, Feptides Derived From Said SSX Gene a
TITLE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556, 1
CURRENT APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 5
LENGTH: 576
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100.0%; Pred. No. 1.7e-184;
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Patent No. 6548064
                                                                                                     Query Match
Best Local Similarity 100.
                        single
nucleic acid
                                            linear
                      STRANDEDNESS:
  ; TYPE: nucle; STRANDEDNES; ; TOPOLOGY: US-09-796-780-1
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                                                            Gaps
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                                Length 576;
                                                           Indels
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                            Score 576; DB 4; L
Pred. No. 1.7e-184;
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APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Williamson, Barbara
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Cancer Associated Antigens and
TITLE OF INVENTION: Cancer Associated Antigens and
TITLE OF INVENTION: Therefor
FILE REFERENCE: L0461/7062
CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09.
BARLIER FILING DATE: 1999-07-15
SEARLIER FILING DATE: 1999-07-15
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                           Mismatches
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                            Query Match
Best Local Similarity 100.0%;
Matches 576; Conservative 0;
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US-09-392-714-17
US-09-833-039A-5
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DB 4; Length 576;

100.0%; Score 576;

Query Match

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scanlar, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Ali O.
APPLICANT: Williamson, Barbara
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Cancer Associated Antigens and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: 1999-09-09
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FELSEQ for Windows Version 3.0
SEQ ID NO: 16
LENGTH: 766
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91.5%; Pred. No. 1.3e-157;
iive 0; Mismatches 49;
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      Pred. No. 1.7e-184;
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; Sequence 16, Application US/09392714A
; Patent No. 6686147
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Local Similarity 100.0%;
nes 576; Conservative C
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Best Local Similarity 91.5
Matches 526; Conservative
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RESULT 9
VS-08-761-119-2
'Sequence 2, Application US/08761119
'Patent No. 5798264
               LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
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US-08-479-328-2
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                                                                     ATGAACGGAGACGACGCCTTTGCAAGGAGACCCCAGGGATGATGCTCAAATATCAGAGAAG
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Patent No. 5698396
GENERAL INFORMATION:
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
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REFERENCE/DOCKET NUMBER: LUD 5410
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 888-2200
TELEFRAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Diskette, 3.5
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5698396
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OPERATING SYSTEM: PC-DOS
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US-08-479-328-2
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APPLICANT: Péreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEB: Felfe & Lynch
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   Length 931;
                                                          Indels
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
Score 496.6; DB 1;
Pred, No. 1.5e-157;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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Uses Thereof

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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                          86.2%; Score 496.6; DB 1; Length 931; 91.5%; Pred. No. 1.5e-157; ive 0; Mismatches 49; Indels 0.
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                                                                                                                     NAME: Hanson, No. 5798264man D. REGISTRATION NUMBER: 30,946
REPESENCE/DOCKET NUMBER: LUD 5410.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
 APPLICATION NUMBER: US/08/761,119
                FILING DATE: 6-DECEMBER-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double-stranded
              6-DECEMBER-1996
                                                                                                                                                                                          TELEPHONE: (212) 688-920
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 931, base pairs
                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 91.5
Matches 526; Conservative
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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US-08-668-128B-2
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Hodgkin's Disease Associated Molecules And

Sequence 2, Application US/08668128B Patent No. 5840568

APPLICANT: Pfreundschuh, Michael TITLE OF INVENTION: Hodgkin's Di

GENERAL INFORMATION:

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                                                                                                                                        ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 496.6; DB 2;
Pred. No. 1.5e-157;
0; Mismatches 49;
                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,128B
FILING DATE: 21-UWB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hanson, No. 5840568man D.
REGISTRATION NUMBER: 30,946
REGISCHENCE/DOCKET NUMBER: 1UD 5441
TELECOMMUNICATION INFORMATION:
TELEPRA: (212) 688-9200
TELEPRA: (212) 839-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/644,116
FILING DATE: 10-MX-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 03-JANUARY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
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Best Local Similarity 91.5%;
Matches 526; Conservative
                                                 Felfe & Lynch
                                                                        805 Third Avenue
                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                            CITY: New York City
STATE: New York
ZIP: 10022
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                                                 ADDRESSEE:
STREET: 80
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US-08-668-128B-2
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159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG 218
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                                                                                        219 AAAGCCTCGGAGAAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA
                                                                                                                                             181 CTAGGITTCAAGGICACCCTCCCACCTTTCATGCGIAGIAAACGGGCTGCAGACTTCCAC
                                                                                                                                                                                                                                          241 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
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Patent No. 6017716
GENERAL INFORMATION:
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: New York City
STREET: New York City
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5410.1
TELECHONICATION INFORMATION:
TELEPAX: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/280,980
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STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-CANUARY 1996
APPLICATION NUMBER: 08/479,3;
FILING DATE: 07-UNE-1995
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-959-625-2
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       CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
                                                                                                    481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
                                                                                                                                                  579 GAACATGCCTGGACCCACAGACTGCGTGAGAGAAAACAGCTGGTGATTTATGAAGAGATC 638
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                                                  519 CCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGATCTGGACCCAAAAGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 THIR'd Avenue
CITY: New York City
STATE: New York
ZIP: 100.22
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó:
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Pred. No. 1.5e-157;
0; Mismatches 49;
                                                                                                                                                                                                  541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
                                                                                                                                                                                                                                               639 Agcgaccergaggaagargacgagraacrecere 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,445
FILING DATE: 04-AUG-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/68,128
FILING DATE: 21-UTNE-1996
APPLICATION NUMBER: 08/64,116
FILING DATE: 10-MAY-1996
APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
FILING DATE: 03-JANUARY-1996
APPLICATION NUMBER: 08/580,980
FILING DATE: 07-UTNE-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5864015man D. REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: LUD 5441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRRACTERISTICS:
LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08905445; Patent No. 5864015; GENERAL INFORMATION:
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ilarity 91.5%;
Conservative (
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Best Local Similarity
Matches 526; Conserv
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TOPOLOGY:
US-08-905-445-2
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US-08-905-445-2
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TOPOLOGY: linear
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TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
TITLE OF INVENTION: And Molecules Identified Thereby
MINMER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York City
STATE: New York
CIPY: New York
STATE: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
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0
                                                                                            Length 931;
                                                                                                                         Indels
                                                                                        Score 496.6; DB 3;
Pred. No. 1.5e~157;
0; Mismatches 49;
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OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERFECT
APPLICATION DATA:
APPLICATION NUMBER: US/09/008,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09008466 Patent No. 6020134 GENERAL INFORMATION:
LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                        86.2%;
ilarity 91.5%;
Conservative
                                            ;
TOPOLOGY: linear
US-08-959-625-2
                                                                                                          al Similarity
526; Conserv
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US-09-008-466-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.2%; Score 496.6; DB 3
Best Local Similarity 91.5%; Pred. No. 1.5e-157
Matches 526; Conservative 0; Mismatches 49
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                                                                                                                                                        NAME: Hanson, No. 6020134man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 100 5410.1
TELECOMONICATION INFORMATION:
TELECOMONICATION: (212) 688-9200
TELETAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 931 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Gouble-Etranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-580-980A-2
; Sequence 2, Application US/08580980A
; Patent No. 6055191
; GENERAL INFORMATION:
; APPLICANT: Pfreundschuh, Michael
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
                                                              FILING DATE: 03-JANUARY-1996
FILING DATE: 03-JANUARY-1996
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
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                      638
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579 GAACATGCCTGGACCCACAGACTGCGTGAGAAAAACAGCTGGTGATTTATGAGAGATC
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                                                                                                                                                                                                                                                                                APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating
TITLE OF INVENTION: A Molecule And Molecules Identified Thereby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 496.6; DB 3;
Pred. No. 1.5e-157;
0; Mismatches 49;
                                                                                                             639 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC
                                                                     541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6103873man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5410
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,453
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TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                  ; Sequence 2, Application US/09053453; Patent No. 6103873
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
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91.5%;
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.5
Matches 526; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-053-453-2
                                                                                                                                                                              RESULT 15
US-09-053-453-2
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           Method For Identifying Or Isolating A Molecule And Molecules Identified Thereby
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STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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Pred. No. 1.5e-157;
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

PEDELICATION NUMBER: US/08/580,980A
FILING DATE: 03-UANUARY-1996
CLASSIFICATION: 435
PRICA PAPLICATION: 435
PRICA PAPLICATION: DATA:

APPLICATION NUMBER: 08/479,328
FILING DATE: 07-UNE-1995
ATTORNEY, AGENT INFORMATION:

NAME: HANGON, NO. 6025191man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5410.1
FELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LINGTH: 931 base pairs
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nucleic acid
EDNESS: double-stranded
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Best Local Similarity 91.5%;
Matches 526; Conservative
                                                                                                  ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
               TITLE OF INVENTION: AM
TITLE OF INVENTION: AM
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: do: TOPOLOGY: linear
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                                     361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                                        481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAAGCAGCTGGTGGTTTATGAAGAGATC 540
                                                                                                                                           579 GAACAIGCCTGGACCACCACGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC 638
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Search completed: March 31, 2004, 17:26:48 Job time : 99 secs

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Sequence 1, Appli
Sequence 5, Appli
Sequence 59, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 1000, Ap
Sequence 1000, Ap
Sequence 1322, Appli
Sequence 402, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
                                                                                                         March 31, 2004, 16:39:19 ; Search time 389 Seconds (without alignments) 5512.734 Million cell updates/sec
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576
1 ATGAACGGAGACGCCTT.....ATGACGAGTAACTCCCCTCG 576
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-833-039-5

US-10-177-277-5

US-10-117-937-599-1

US-09-849-602-13

US-10-207-655-84

US-10-117-937-6

US-09-834-531-1000

US-09-954-531-1000

US-09-954-531-1302

US-10-159-563-402

US-10-159-563-402

US-09-958-856-2

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Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 1, Appli Sequence 1, Appli Sequence 106782, Sequence 24594, A Sequence 23951, A Sequence 23951, A Sequence 33096, A Sequence 1148783, Sequence 114514, Sequence 114514, Sequence 114514, Sequence 114515, Sequence 322431, Sequence 322431, Sequence 6728, Appl Sequence 68497, A Sequence 58497, A Sequence 18465, A Sequence 18465, A Sequence 114770, Sequence 18465, A Sequence 18965, A Sequence 1817, Appl Sequence 187, Appl Sequence 187, Appl Sequence 187, Appl Sequence 187, Appl	Ugur, Tsang, Solam; r; Pfreundschuh, Michael; cules Encoding SSX orage
US-09-833-039-1 US-10-177-277-1 US-10-027-652-106782 US-10-027-632-106782 US-10-029-386-23951 US-10-029-386-23951 US-10-027-632-33096 US-10-027-632-33096 US-10-027-632-148783 US-10-027-632-148783 US-10-027-632-148783 US-10-027-632-148783 US-10-027-632-14514 US-10-027-632-14818 US-10-027-632-14818 US-10-027-632-14818 US-10-027-632-14818 US-10-027-632-14818 US-10-027-632-14818 US-10-027-632-14818 US-10-027-632-14818 US-09-814-353-84 US-10-027-632-138181 US-10-027-632-138181 US-10-029-884-18181 US-10-029-884-18181 US-10-029-884-18181 US-10-029-884-18181 US-10-029-884-181	MENTS Ozlem; Sahin, Ug Kmuth Alexander; seng Heic Acid Molecu: Uses Thereof rski L.L.P. inch, 144 kb stor inch, 15,856 is 856 is 856 is 856
	099758E 57Al. 0.; Tu Matthew I Solate Family Members Members SS: SS: SS: Clty AM: AV: NM: NM: SM: SM: SM: SM: SM: SM: SM: SM: SM: S
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480 308.6 1008.6 1111.4 1111.4 1111.4 101.6 101.	ALIGN SSULT 1 Sequence 1, Application US/09975856 Publication No. US20030023057A1 GENERAL INFORMATION: APPLICANT: Gure, Ali O.; Tureci, Scallar, Matthew J.; Lloyd J.; Chen, Yao-T TITLE OF INVENTION: ISOlated Nuc- Family Members And Pamers And 1 NUMBER OF SEQUENCES: 14 CORENERS: 66 Fith Avenue STREET: 66 Fith Avenue CITY: New York City ZIP: 10103 COMPUTER: IBW OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect COMPUTER: IBW OPERATING SYSTEM: BC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: 05/09/97 FILING DATE: 11-Oct-2001 CLASSIFICATION DATA: APPLICATION NUMBER: 03/96,7 FILING DATE: 10-Oct-30.01 ATTORNEY/AGENT INFORMATION: NAME: Hanson, NO. US20030023 REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: 101 TELECOMMUNICATION INFORMATION: NUMBER: Hanson, NO. US20030023 REFERENCE/COCKET NUMBER: 101 TELECOMMUNICATION INFORMATION: TELEPAN: (212) 752-5558 INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Freundschuh, Michael
TITLE OF INVENTION: Throw Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                       Length 576;
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                                                                                                                                                                                                            Score 576; DB 10;
Pred. No. 2.8e-174;
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                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
INCE CHARACTERISTICS:
LENGTH: 576 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
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; Publication No. US20030175960A1
; GENERAL INFORMATION:
                                                                                                                                                                                                               100.0%;
                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                  Local Similarity 100.
1es 576; Conservative
     SEQUENCE
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US-09-833-039-5
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Sequence 5, Application US/10177277

Publication No. US20030185844A1

GENERAL INFORMATION:

APPLICANT: Sahin, Ugur

APPLICANT: Sahin, Ugur

APPLICANT: Steundschuh, Michael

APPLICANT: Stevanovic, Stefan

ITLLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determ:

ITLLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene

ITLLE OF INVENTION: Gene, and Uses Thereof

ITLLE OF INVENTION: Gene, and Uses Thereof

FILE REFERRNCE: LUD 5556.1

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US/09/344,040

PRIOR APPLICATION NUMBER: US 09/105,839

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26

PRIOR PRILOR APPLICATION NUMBER: US 09/105,839

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26
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                                                                                                                                                                               Indels
                                                                                                                                  Score 576; DB 10;
Pred. No. 2.8e-174;
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                                                                                                                         Query Match
100.0%; Score 576; D
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 576; Conservative 0; Mismatches
                                      ; TYPE: DNA; ORGANISM: Homo sapiens US-09-833-039-5
SEQ ID NO 5
LENGTH: 576
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US-10-177-277-5
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180 240 300

360 420 420 480 540 540

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100.0%; Score 576; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-174;
Matches 576; Conservative 0; Mismatches 0;
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Publication No. US20030165834A1

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew J.

APPLICANT: Stanlan, Matthew J.

APPLICANT: Stockert, Elisabeth

APPLICANT: Chen, Yao-Teson

TITLE FOF INVENTION: Colon Cancer Antigen Panel

FILE REFERENCE: L0461/7105(JRV)

CURRENT APPLICATION NUMBER: US/09/849,602

UNDRER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.0
             ; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 599
; LENORH: 576
                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
US-10-117-937-599
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ORGANISM: Homo sapien
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LENGTH: 766
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                                                                                                                                                             Length 576;
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                                                                                                                                                     100.0%; Score 576; DB 14;
100.0%; Pred. No. 2.8e-174;
cive 0; Mismatches 0;
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APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM, 027A
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR PELING DATE: 2001-01-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 599, Application US/10117937; Publication No. US20030220239A1
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 5
LENGTH: 576
                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 576; Conservative
                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-10-117-937-599
                                                                                                               US-10-177-277-5
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                                                      152 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGGTGGGGAAAAGATG
                                                                                                                                                                                212 AAAGCCTCGGAGAAAATCTTCTATGTGTATATGAGAAGAAGTATGAGGCTATGACTAAA
                                                                                                                                                                                                                                             CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
                                                                                                                   121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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Sequence 6, Application US/10117937
Publication No. US2003022039A1
SEQUENCE INFORMATION:
APPLICANT: SIMARD, JOHN, J.L.
APPLICANT: BIMARD, DAVIG, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM 027A
CURRENT APPLICATION NUMBER: US/01/117,937
CURRENT PILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/3437,017
PRIOR APPLICATION NUMBER: US 60/3437,017
PRIOR APPLICATION NUMBER: US 60/3437,017
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
SPRIOR PILING DATE: 2001-11-07
SPRIOR PILING DATE: 2001-11-07
SPRIOR PILING DATE: 2001-04-06
SPRIOR PILING DATE: 2001-04-06
SPRIOR PILING DATE: 2001-01-07
SPRIOR PILING DATE: 2001-01-07
SPRIOR PILING DATE: 2001-01-07
SPRIOR PILING DATE: 2002-07
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US-10-117-937-6
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                                                                                                                                                                                                                                                                                                      ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAAGATG
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                                                                                                                         1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
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Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledderter, Jeffrey A.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069, 401C1

CURRENT APPLICANION NUMBER: US/10/207,655

NUMBER OF SEQ ID NOS: 426

SOFTWARE: Patentin version 3.0
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                   Length 766
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Pred. No. 1e-148;
0; Mismatches 49; Indels 0;
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                   DB 10;
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            Score 496.6; I
Pred. No. 1e-14
0; Mismatches
         tch 86.2%;
al Similarity 91.5%;
526; Conservative
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Best Local Similarity 91.5%;
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ORGANISM: Homo sapiens
      Query Match
Best Local Similarity
Matches 526; Conserv
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US-10-207-655-84
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APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sherundschuh, Michael
APPLICANT: Pireundschuh, Michael
APPLICANT: Pireundschuh, Michael
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determi
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
TITLE OF INVENTION: Gene, and Uses Thereof
TITLE OF INVENTION: Gene, 2002-06-21
CURRENT APPLICATION NUMBER: US/10/177,277
CURRENT FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
    ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAGAGAGGGGAAAAGATG 218
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                                                                      AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
                                                                                                                                                          CTAGGITICAAGGICACCTCCCACCTTTCATGCGIAGTAAACGGGCTGCAGACTTCCAC
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Pred. No. 1.1e-148;
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Matches 526;
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APPLICANT: Tured:, Ozlem
APPLICANT: Tured:, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Turer Associated Peptide and Uses Thereof
FILE REPRENCE: LUD 5622.1
FILE REPRENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US 09/409,455
FRIOR FILING DATE: 2001-04-12
FRIOR PPLICATION NUMBER: US 09/409,455
FRIOR FILING DATE: 1999-05-30
FRIOR FILING DATE: 1999-06-26
FRIOR APPLICATION NUMBER: US 09/105,839
FRIOR FILING DATE: 1998-06-26
FRIOR APPLICATION NUMBER: US 08/851,130
FRIOR FILING DATE: 1997-05-05
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Pred. No. 1.1e-148;
0; Mismatches 49;
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Matches 526; Conservative
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### APPLICANT: Weaver. Zoe

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Car

TITLE OF INVENTION: Gene Sets

FITLE OF INVENTION: Gene Sets

FILE REPRENCE: 689290-77

CURRENT PILING DATE: 2002-05-02

FRIOR PRILING DATE: 2000-09-18

FRIOR FILING DATE: 2000-09-20

FRIOR PELING DATE: 2000-09-20

FRIOR APPLICATION NUMBER: US/60/234,034

FRIOR FILING DATE: 2000-09-20

FRIOR PELING DATE: 2000-09-20

FRIOR PELING DATE: 2000-09-22

FRIOR SELING DATE: 2000-09-22

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Patent No. US20020165180A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1309)
OTHER INFORMATION: n=a,t,g or c
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Patent No. US20020165180A1

GENERAL INFORMATION:

APPLICANT: Weaver. Zoe

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION: Gene Sets

TITLE OF LINVENTION: Gene Sets

TITLE OF LINVENTION: Gene Sets

FILE REFERENCE: 689290-77

CURRENT FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOFFWARE: PATENTIN VENESION 3.0
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Pred. No. 1.4e-148;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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Best Local Similarity 91.5%;
Matches 526; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)...(1309)
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US-09-954-531-1000
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Sequence 2, Application US/09975856
Publication No. US20030023057A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
Scanlan, Matthew J.; Knuth Alexander; Pfreundschuh, Michael; Old,
Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX
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FILING DATE: 11-Oct-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/796,780
FILING DATE: 2001-03-01
  0; Mismatches
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COMPACE: IBM
COPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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    526; Conservative
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US-09-975-856-2
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PUBLICATION No. US20040009154A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Paul
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS;
FILE REPERRANCE: 11613.560711,
CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
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                                                                               Indels
                                      Score 496.6; DB 9;
Pred. No. 1.4e-148;
0; Mismatches 49;
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Pred. No. 2.1e-148;
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91.3%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 402
LENGTH: 1249
                                        Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
      US-09-954-531-1392
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US-10-159-563-402
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                                                                                                                                                                                                                                Score 482.2; DB 10;
Pred. No. 3.7e-144;
0; Mismatches 58;
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               'n
            US20030023057A1man
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APPLICANT: Sahin, Ugur
APPLICANT: Serundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
            NAME: Hanson, No. US20030023057Alm
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5480
                                                                                                                                                                                        ς,
                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // Sequence 6, Application US/09833039
// Publication No. US20030175960A1
// GENERAL INFORMATION:
                                                                                                                             LENGTH: 576 nucleotides
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 89.9
Matches 517; Conservative
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US-09-833-039-6
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APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determ:
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
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Pred. No. 3.7e-144;
0; Mismatches 58;
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PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR PLING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 6
LENGTH: 576
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Publication No. US20030185844A1
GENERAL INFORMATION:
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89.9%;
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Best Local Similarity 89.9
Matches 517; Conservative
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US-09-833-039-6
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Pred. No. 3.7e-144;
0; Mismatches 58; Indels 0;
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FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/10/177,277
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/9/344,040
PRIOR FILING DATE: 1990-06-25
PRIOR FILING DATE: 1990-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
NUMBER OF SQ ID NOS: 132
SEQ ID NO 6
SEQ ID NO 6: 100 6
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.9%;
Matches 517; Conservative
                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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METJA HUMAN RABIT HUMAN

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Q61967 Q9h2p0 P04932 P04933 O75467 Q16587 P095201 P11827

MSP1 PLAFW Z324 HUMAN ZN74 HUMAN

RRPO_BWYVF Z205_HUMAN

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homo sapien

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(without alignments)
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           Compugen Ltd.
                             using frame_plus_n2p model
    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compuc
                                                                                                                                        Total number of hits satisfying chosen parameters:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                US-09-975-856-1
1025
                            protein search,
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                                                                Title:
Perfect score:
                                                                                        Scoring table:
                           nucleic
                                                                            Sequence:
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SSX4 HUMAN RESULT 1

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Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; Last sequence update)
Last annotation update) 188 AA Created) 15-JUL-1999 (Rel. 38, 15-JUL-1999 (Rel. 38, 10-OCT-2003 (Rel. 42, Homo sapiens (Human). SSX4 HUMAN O60224; Q9UJU9; 15-JUL-1999 (Rel SSX4 protein.

SEQUENCE FROM N.A. MEDLINE=98021352; PubMed=9378559; Gure A.O., Tuereci O., Sahin U., Tsang S., Scanlan M.J., Jager E., Kunth A., Pfreundschuh M., Old L.J., Chen Y.-T.; Transcribed in normal "SSX: a multigene family with several members transcribed in normal testis and human cancer."; Int. J. Cancer 72:965-971(1997).

SEQUENCE FROM N.A.

TISSUB-Urinary bladder;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

WELTARLED R. L., Colling F. S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K., Antschenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mazny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting M., Machan J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A. Schein J.E., Jones S.J.M., Marra M.A.;

ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Command line parameters:
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-DB=SwisSPTOt_42_OFMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPEXT=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	060224 homo sapien Q99909 homo sapien	Q16385 homo sapien Q16384 homo sapien	homod	рошоц	O70173 rattus norv		P16549 sus scrofa			P17036 homo sapien	Q62396 mus musculu	Q61751 mus musculu	
SUMMARIES	SSX4_HUMAN SSX3_HUMAN	SSX2_HUMAN SSX1_HUMAN	SSX5_HUMAN ZN75_HUMAN	Z398_HUMAN	PK3G RAT	FMO1_CANFA	FMO1_PIG	REP1_HUMAN	SX11_CHICK	ZN38_HUMAN	ZF92 MOUSE	TC17 MOUSE	WR61_ARATH
% Query Match Length DB	188 1 188 1	88 11	188 1 289 1	642 1	05 1	531 1	531 1	44 1	96 1	46 1	488 1	572 1	B0 1
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Matches:
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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EMBL; U90840; AAC05819.1; -.
Genew; HGNC:11337; SSX3.
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  Generation and initial analysis of more than 15,000 full-length
                                                                                  SEQUENCE OF 1-155 FROM N.A.
Blechbechmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel Meindl A., Rosenthal A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Could act as a modulator of transcription.
-! SIMILARITY: Belongs to the SSX family.
-! SIMILARITY: Contains 1 KRAB-related domain.
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InterPro; IPR003655; KRAB_related.
InterPro; IPR003655; KRAB_related.
Pfam, PF01352; KRAB; 1.
PR031TE; PS0806; KRAB; 1.
PR051TE; PS0806; KRAB, RELATED; 1.
Multigene family; Transcription regulation.
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20 83 KRAB-RELATED.
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                      human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches:
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EMBL; AF196972; AAF06796.1; -.
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Best Local Similarity:
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-!- FUNCTION: Could act as a modulator of transcription.
-!- SIMILARITY: Belongs to the SSX family.
-!- SIMILARITY: Contains 1 KRAB-related domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Leeuw B., Balemans M., Geurts van Kessel A.; "A novel Kruppel-associated box containing the SSX gene (SSX3) on human X chromosome is not implicated in t(X;18)-positive synovial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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|LeuGlyPheLysAlaIleLeuProSerPheMetArgAsnLysArgValThrAspPheGln 80
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                                                                                  AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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                                        ATGAACGGAGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG
                                                                                                     21 IleGlnLysAlaPheAspAspIleAlaLysTyrPheSerLysGluGluTrpGluLysMet
                                                                                                                                                LysvalserGluLysilevalTyrvalTyrMetLysArgLysTyrGluAlaMetThrLys
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MEDLINE=95292974; PubMed=7539744;
Crew A.U. Clark J., Fisher C., Gill S., Grimer R., Chand A.,
Crew A.U. Glark T., Cooper C.S.;
Shipley J., Gusterson B.A., Cooper C.S.;
"Fusion of SYT to two genes, SSXI and SSX2, encoding proteins with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology to the Kruppel-associated box in human synovial sarcoma.";
EMBO J. 14:2333-2340(1995).
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSX2 HUMAN STANDARD; PRT; 188 AA.
016385; 016404; 0961P7;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
SSX2 protein (Synovial sarcoma, X breakpoint 2) (SSX) (HOM-MEL-40)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Gaps:
                  US-09-975-856-1 (1-576) x SSX3 HUMAN (1-188)
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95038816; PubMed=7951320; Clark J., Rocques P.J., Crew A.J., Gill S., Shipley J., Chan A.M.-L., Gusterson B.A., Cooper C.S.; "Identification of novel genes, SYT and SSX, involved in the t(X:18) [pll.2;qill.2) translocation found in human synovial sarcoma."; Nat. Genet. 7:502-508(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         de Leeuw B., Balemans M., Olde Weghuis D., Geurts van Kessel A., "Identification of two alternative fusion genes, SYT-SSX1 and SYT-SSX2, in t(X,18)(pll.2;qll.2)-positive synovial sarcomas."; Hum. Mol. Genet. 4:1099(1995).
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Fligman I., Lonardo F., Jhanwar S.C., Gerald W.L., Woodruff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 111-188 FROM N.A. (SSXT-SSX2 FUSION PROTEIN) TISSUE-Synovial sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 68-116 FROM N.A. (SSXT-SSX2 FUSION PROTEIN)
MEDLINE=96094743; PubMed=7495284;
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EMBL; S79994; ABB35674.1; ALT_INIT.
PIR, S55058; S55058.
Genew; HGNC:11336; SSX2.
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MEDLINE=95384157; Pubmed=7655467;
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121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                    181 CTAGGITTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
                                                                                                                                                                                                                                                                                                                                                                                              GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 PheGlyArgLeuGlnGlyIleSerProLysIleMetProLysLysProAlaGluGluGly 120
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                                                                                                                                                                                                                                                                                                                                                                      ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAG
                                                                                                                                                                                                                                                                  MetAsnGlyAspAspAlaPheAlaArgArgProThrValGlyAlaGlnileProGluLys
                                                                                        BREAKPOINT FOR TRANSLOCATION TO FORM THE SXT-SXZ PUSION PROTEIN (RARE).
BREAKPOINT FOR ITANSLOCATION TO FORM THE SXXT-SXXZ FUSION PROTEIN.
        GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS
                InterPro; IPR01909; KRAB.
InterPro; IPR018655; KRAB.
InterPro; IPR01352; KRAB.
1.
SMART; SM00349; KRAB, 1.
PROSITE; PSS0806; KRAB. RELATED; 1.
Chromosomal translocation; Proto-oncogene; Multigene family;
                                                                                                                             R -> P (IN REF. 2; AAH07343).
BF5D18AA5F45B1B1 CRC64;
                                                                                                                                                                  188
150
12
26
0
                                                                                                                                                                Length:
Matches:
Conservative:
                                                                                                                                                                                             Mismatches:
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                                                                                  KRAB-RELATED.
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                                                                                                                                       21620 MW;
                                                                                                                                                                3.66e-71
798.00
86.17%
79.79%
                                                                       Transcription regulation.
DOMAIN 20 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                           111
                                                                                                                             169
                                                                                                                            169 :
188 AA;
                                                                                                                                                                                                                              US-09-975-856-1 (1-576)
                                                                                                                                                                                            Local Similarity:
                                                                                          89
                                                                                                           110
                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q16384;
15-DEC-1998 (
15-DEC-1998 (
MIM; 300192;
                                                                                                                                                       Alignment Scores:
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                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                  Query Match:
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ID SSX1_HU
AC Q16384;
DT 15-DEC-
DT 15-DEC-
                                                                                                           SITE
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There are no restrictions on its
ng as its content is in no way
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RA MEDIJURE-22388857; PubMed=12477932;

RA Strausberg R.D., Feingold E.A., Grouse I.H., Derge J.G.,

RA Altanner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenkor L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Nilalon D.K., Muuxry D.M., Sodergram B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butkesley R.W., Touchman J.W., Gremu E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J. Jones S.J.M., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length

RI human and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license ascement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYT-SSX2, in t(K;18) (pl1:2;quil.2)-positive synovial sarcomas.";

Hum. Mol. Genet. 4:1097-1099(1995).

Hum. Mol. Genet. 4:1097-1099(1995).

-i-FUNCTION: Could act as a modulator of transcription.

-i-FUNCTION: Could act as a modulator of transcription.

Expressed at low level in thyroid. Not detected in tonsil, colon, lung, spleen, prostate, kidney, striated and smooth muscles.

Dispute a prostate, kidney, striated and smooth muscles.

Could act and especifically found in more than 80% of detected in mesenchymal and epithelial cell lines. Not detected in mesenchymal and epithelial cell lines.

Couls act and produces the SSXT-SSX1 or SSXT-SSX2 fusion products. These hybrid proteins are probably responsible for transforming activity, Heterogeneity in the position of the breakpoint can occur (low frequency).

Couls all MILARITY: Contains 1 KRAB-related domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE=95292974: Clark J., Fisher C., Gill S., Grimer R., Chand A., Crew A.J., Clark J., Fisher C., Gill S., Grimer R., Chand A., Shipley J., Gusterson B.A., Cooper C.S.; "Fusion of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma."; EMBO J. 14:2333-2340(1995).
                                                                                                                                                                                           Euteleostomi;
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                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
sarcoma, X breakpoint
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Last
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                                  SSX1 protein (Synovial
42
                                                                                                                                (Human)
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                     sapiens
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EMBL; X86174; CAA60110.1; -. EMBL; BC001003; AAH01003.1;

(Rel. 37, Created) (Rel. 37, Last sequence update)

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O60225; Q96AW3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAsnAspPheAspAsnAspHisAsnArgArglleGlnValGluHisProGlnMetThr 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetAsnGlyAspAspThrPheAlaLysArgProArgAspAspAlaLysAlaSerGluLys
                                                                                                                                                                                                           SSXT-SSXI FUSION PROTEIN (RAKE).
BREAKPOINT FOR TRANSLOCATION TO FORM THE SSXT-SSXI FUSION PROTEIN.
; E440D1B2AE3AE9F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProProGlyLysAlaAsnIleSerGluLysIleAsnLysArgSerGlyProLysArgGly
                                                                                                                                                                                                  BREAKPOINT FOR TRANSLOCATION TO FORM THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                         PROSITE; PS50806; KRAB RELATED; 1.
Chromosomal translocation; Proto-oncogene; Multigene family;
          PIR, $55057; $55057.

Genew; BGNC:11335; SSXI.

MIN, 312805.

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0003714; F:transcription co-repressor activity; TAS.

InterPro; IPR001909; KRAB.

InterPro; IPR0015655; KRAB_related.

Ffam; PF01352; KRAB; 1.

SWART; SW00349; KRAB; 1.
                                                                                                                                                                                                                                                                                                 188
149
9 0
0 0
                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                          8.96e-70
784.00
84.04%
79.26%
  AAB35378.1;
                                                                                                                                                                     Transcription regulation.

DOMAIN 20 83
SITE 62 63
                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                           110
879325;
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SSX5_HUMAN
ID SSX5_HUMAN
                                                                                                                                                                                                                                                       SEQUENCE
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188 AA

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Strausborg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Rausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Butetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Butetow K.H., Schaefer C.F., Bhat M.K., Ra Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F., Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Repersion M., Jodin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Rosak S.A., McEwan P.J., McGernan K.J., Malek J.A., Gay L.J., Hulyk S.W., Raha S.S., Wolferd W., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Multing M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G., Rateefield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Nenezation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(202).

FIGURAL ALTERNATIVE PRODUCTS:
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InterPro; IPR003655; KRAB.
InterPro; IPR003655; KRAB.
Fam; PF01352; KRAB; 1.
SMART; SM00349; KRAB; 1.
SMART; SM00349; KRAB; 1.
Multigene family; Transcription regulation; Alternative splicing.
DOMAIN 20 83 KRAB-RELATED.
DOMAIN 20 83 K -> KHPWRQVCDRGIHLVNLSPFWKVGREPASSIKALLC
                                                                                                                                                                                                                                                        Gure A.O., Tuereci O., Sahin U., Tsang S., Scanlan M.J., Jager E., Knuth A., Pfreundschuh M., Old L.J., Chen Y.T., "SSX: a multigene family with several members transcribed in normal testis and human cancer.";
                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note=No experimental confirmation available; SIMILARITY: Belongs to the SSX family. SIMILARITY: Contains 1 KRAB-related domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=060225-2; Sequence=VSP_006274;
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                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Skin;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98021352; PubMed=9378559;
                                                                                                                                                                                                                                                                                                                                           Int. J. Cancer 72:965-971(1997).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U90842; AAC05821.1; -. EMBL; BC016640; AAH16640.1;
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MIM; 300327; -.
              15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
10-OCT-2003 (Rel. 42,
                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI TaxID=9606;
                                                                            SSX5 protein.
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Pred. No.:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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SEQUENCE FROM N.A.
TISSUE-Lung fibroblast;
MEDLINE-94116987; PubMed=8288223;
Villa A., Zucchi I., Pilia G., Strina D., Susani L., Morali F.,
GRGEAR (in isoform 2).
/FTId=VSP 006274.
P -> Q (IN REF. 2).
AD2A3096931C5E37 CRC64;
                                                                                                         1188
441
84
80
0
                                                                                                       Length:
Matches:
Conservative:
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Indels:
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zhor finger protein 75.
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21628 MW;
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                                 184 J
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                                                                                                                                                           Similarity:
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                                                                                                                                        Percent Similarity:
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P51815;
01-OCT-1996 (
01-OCT-1996 (
10-OCT-2003 (
                                                                                   Alignment Scores:
                                   CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R GO; GO:0005634; C:nucleus; NAS.

R GO; GO:0006270; F:nucleus; NAS.

R GO; GO:0008270; F:nucleus; NAS.

R GO; GO:0008270; F:nucleus; NAS.

R GO; GO:0008270; F:nucleus; NAS.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.

InterPro; IPRO01089; Znf_C2H2.

InterPro; IPRO07086; Znf_C2H2.

R Pfam; PF01096; zf_C2H2; S.

R PRINTS; PR00048; ZINCFINGER.

R PROOFF PRO000043; Znf_C2H2; S.

R RART; SM00349; KRAB; 1.

R SMART; SM00349; KRAB; 1.

R PROSTIE; PS500058; ZINC_FINGER_C2H2 1; S.

R PROSTIE; PS500028; ZINC_FINGER_C2H2 2; S.

R PROSTIE; PS50157; ZINC_FINGER_C2H2 2; S.

R Transcription; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                              [2] SEQUENCE OF 139-289 FROM N.A. BAZE N., ROSALÍ M., ROCCHÍ M., Marino M., Archidiacono N., Franze N., Rosatí M., Rocchí M., Ballabio A., Grimaldí G., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
Patrosso C., Frattini A., Lucchini F., Repetto M., Sacco M.G., Zoppe M., Vezzoni P., "ZNF75: isolation of a cDNA clone of the KRAB zinc finger gene subfamily mapped in YACs 1 Mb telomeric of HPRT."; Genomics 18:223-229(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
C2H2-TYPE 5.
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23
23
43
5
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-!- SIMILARITY: Contains 5 C2H2-type zinc fingers.
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Indels:
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PIR, A48913, A48913.
HSSP; P25490; 1ZNM.
Genew; HGNC:13145; ZNF75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S67970; AAB29696.1; -.
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11.07%
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Score:
     A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Itachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blata N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Mang J., Heibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Morlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W., Wurmy D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Nillalon D.K., Munny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",
                                                                                                                                                                                                                                                408
                               249
                                                                                  264
                                                                                                                                                                  100
                                                                                                                                                                                          -----AGAATCTTCCCGAAGATCATGCCCAAGAAGCCA 348
                                                                                                                                                                                                                  101 AspThrHisSerValGlnLysTrpHisArgAlaPheProArgLysLysArgLysLysPro 120
                                                                                                                                                                                                                                                              9
                                                                                                             80
36 LysThrLeuTyrAsnAspValMetGlnAspIleTyrGluThrVallleSerLeuGlyLeu 55
                                                                                                         ThrdlyAshAspHisProlleSerValSerThrSerGluIleGlnThrSerGlyCysGlu
                                                                                                                                                             81 ValSerLysLysThrArgMetLysIleAlaGlnLysThrMetGlyArgGluAsnProGly
                           AAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCACGGGAATGAT
                                                          ---AsnAsp
                                                                                                                                                                                                                                              GCAGAGGAAGAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conroy A.T., Sharma M., Holtz A.E., Wu C., Sun Z., Weigel R.J.;
"A novel zinc finger transcription factor with two isoforms that are
differentially repressed by estrogen receptor-alpha.";
J. Biol. Chem. 277:9326-9334 (2002).
                                                                                                                                                                                                                                                                                                                                                                                 Z398_HUMAN STANDARD, PRT; 642 AA.
68TD17, 68TD18; 09PZ7; 09UDV8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
Zinc finger protein 398 (Zinc finger DNA binding protein p52/p71)
ZNF398 OR ZERG OR KIAA1339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bemis G., Langston Y., Tucci S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                    265 ---AACCACAGGAATCAGGTTGAACGTCCTCAGATGACTTTCGGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=21883346; Pubmed=11779858;
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MEDLINE=22388257; PubMed=12477932;
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SEQUENCE FROM N.A. (ISOFORM 1).
                                                                               250 TTTGGTAACGATCGA--
                                                       LysLeuLys---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SIMILARITY: Contains 1 KRAB domain.
-:- CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                              SEQUENCE OF 234-642 FROM N.A.

MEDLINE=20181126; PubMed=10718199;

MEDLINE=20181126; PubMed=10718199;

Magage T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. XVI

The complete sequences of 150 new cDNA clones from brain which code

for large proteins in vitro.";

DNA Res. 7:65-73(2000).

-!- TUNCTION: Function as a transcriptional activator.

-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:18373; ZNF398.

Go; GO:0005634; C:nucleus; NAS.

GO; GO:0016563; F:transcriptional activator activity; NAS.

GO; GO:0006355; F:transcription of transcription, DNA-dependent; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=Q@TD17-2, % Sequence=VSP 006926;
INDUCTION: By estrogen receptor alpha.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50805; KRAB; 1.
PROSITE; PS50805; ZINC FINGER C2H2 1; 7.
PROSITE; PS50157; ZINC-FINGER C2H2-2; 8.
Transcription regulation; Activator; DNA-binding; Zinc-finger;
Metal-binding; Nuclear protein; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69AA38FCD84FF633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (in isoform 2).
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=p71;
IsoId=Q8TD17-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C2H2-TYPE (ATYPICAL)
C2H2-TYPE (DEGENERAT
C2H2-TYPE.
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Matches:
Conservative:
Mismatches:
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C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AC004890; AAD45824.1; ALT_SEQ.
EMBL; BC043295; AAH43295.1; -.
EMBL; AB037760; BAA92577.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001909; KRAB.
InterPro; IPR001090; KRAB.
Fram, PF01322; KRAB; 1.
Pfam; PF01322; KRAB; 1.
Pfam; PF00096; zf-C2H2; 8.
ProDom; PD000009; znf_C2H2; 2.
SMART; SM00149; KRAB; 2.
SMART; SM00149; KRAB; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY049744; AAK92789.1; -. EMBL; AY049743; AAK92788.1; -.
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41.60%
24.80%
                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2; Synonyms=p52;
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Best Local Similarity:
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595 AA;
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                                                                                                                         180 IleSerMetAspTyrAlaileAsnGlnProAspValLeuSerGlnIleGlnProGluGly 199
                                                                                                                                                                                                                                                                                                                         |||
| GluPro---GlyIleSerThrSerAspIleLeuSerTrpIleLysGlnGluGluGluBro 239
                                                                                  LysValProValAlaPheAspAspValSerIleTyrPheSerThrProGluTrpGluLys 159
                                                                                                                                                                                                                                                                                                           381
                                                                                                          118 ATGAAATCCTCGGAGAAATCGTCTATGTG---TATATGAAGCTAAACTATGAGGTCATG 174
                                                                                                                                                         175 ACTAAACTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGAC 234
                                                                                                                                                                                                         TICCACGGGAATGATTITGGTAACGATCGAAACCACAGGAATCAGGTIGAACGTCCTCAG 294
                                                                                                                                                                                                                                                         295 ATGACTTTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koike T., Sawada Ki K.;
"Molecular cloning and characterization of a KRAB-containing zinc
finger protein, ZNF317, and its foforms.";
Blochem. Blophys. Res. Commun. 288:771-779 (2001).
-!- FUNCTION: May function as a transcription factor. May play an
important role in erythroid maturation and lymphoid proliferation.
-!- SUBCELLUIAR LOCATION: Nuclear (Probable).
                                                          AAGTTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGAAAAGAGTGGGAAAAG
                                                                                                                                                                                                                            200 GluHisAsnThrGlu------AspGlnAlaGlyProGluGluSerGlu------
                                                                                                                                                                                                                                                                                  ------IleproThrAspProSerGlu
                                                                                                                                                                                                                                                                                                           ----AAGGAAGTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE SPECIFICITY: Isoforms land 3 are ubiquitously expressed. Isoforms 3 and 4 are expressed only in lymphocytes, spleen, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZNF317.

ZNF317.

ZNF317.

Floo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
MEDLINE=21547764; PubMed=11688974;
Takashima H., Nishio H., Wakao H., Nishio M., Koizumi K., Oda A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=ZNF317-1;
IsoId=Q96PQ6-2; Sequence=VSP_006916;
Name=3; Synonyms=ZNF317-3;
IsoId=Q96PQ6-3; Sequence=VSP_006915, VSP_006916;
   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=4;
Name=2; Synonyms=ZNF317-2;
IsoId=Q96PQ6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                             2317_HUMAN STANDARD; PRT; 595 AA. Q96PQ6; Q96PM1; Q96PT2; 28-FBB-2003 (Rel. 41, Created) Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=4; Synonyms=ZNF317-4;
Isold=Q96PQ6-4; Sequence=VSP 006915;
TISSUE SPECIFICITY: Isoforms 1 and 3 as
  Indels:
                                  US-09-975-856-1 (1-576) x Z398_HUMAN (1-642)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINGER PROTEINS.
SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                         GAAGAAAATGGTTTG-----
                                                                                                                                                                                                                                                                                                                                                                        :::
240 GlnValGlyAlaPro 244
                                                                                                                                                                                                                                                                                                                                                       382 GAGGCATCTGGCCCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein 317
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AAAATCGTCTATGTGTATATGAAGCTA---AACTATGAGGTCATGACTAAACTAGGTTTC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::|||
99 GlnValGlyLysProSerLeuIleSerHisLeuGluGluGluGluGluBroArgThrGlu 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GluArgGlyAlaHisGlnGlyAlaCysAlaAspTrpGluThrProSerLysThrLysTrp 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 AGCCTC-----CAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAGGAAGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AAGGTCACCTCCCACCTTTCATG---CGTAGTAAACGGGCTGCAGACTTCCACGGGAAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 ArglyeleuTyrLysAspValMetLeuGluAsnTyrSerAsnLeuThrSerLeuGlyTyr 98
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF0152; KRAB; 1...
Pfam; PF0152; KRAB; 1...
Pfam; PF00096; zf-CH2; 13.
SMART; SM00349; KRAB; 1...
SMART; SM00349; KRAB; 1...
PROSITE; PS50805; KRAB; 1...
PROSITE; PS50805; KRAB; 1...
Transcription regulation; Zing-finger; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 3 and isoform 4)./FTId=VSP_006915.
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Matches:
Conservative:
Mismatches:
Indels:
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DOMAIN 57 128 KRAB.
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C2H2-TYPE.
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Missing (i
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                                                                                                                                                                                          EMBL; AF275255; AAL29188.1; --
EMBL; AF148135; AAL29182.1; --
EMBL; AF307095; AAL29190.1; --
EMBL; AF307097; AAL29191.1; --
PIR; JC7779; JC7779.
InterPro; IPR001909; KRAB.
InterPro; IPR001909; ZAF210.1
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94.00
47.62%
30.48%
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SMART; SM00146; PI3Kc; 1.
                                                                                                                                          SEQUENCE
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                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in n way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE=Regenerating liver;

MEDLINE=98184888; PubMed=9516481;

MEDLINE=98184888; PubMed=9516481;

MEDLINE=98184888 T. S., Owada Y., Sakagami H., Goto K.,

Suzuki M., Matsuno S., Kondo H.;

"A novel class II phosphoinositide 3 kinase predominantly expressed in
the liver and its enhanced expression during liver regeneration.";

J. Biol. Chem. 273:7731-7736(1998).

-i- FUNCTION: IN VITRO, PHOSPHORYLATES PIDINS AND PIDINS4P BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositel 4-phosphate 3-kinase C2 domain-containing polypeptide (EC 2.7.1.154) (Phosphoinositide 3-Kinase-C2-gamma)
(PtdIns-3-kinase C2 gamma) (P13K-C2gamma).
                                                                                                       1505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008938; ARM.
InterPro; IPR000008; C2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR008973; P14 kinase.
InterPro; IPR002420; P13K_C2.
InterPro; IPR002420; P13K_C2.
InterPro; IPR001263; P13K_ras_bind.
InterPro; IPR001263; P13Ka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00168; C2; 1.
Pfam; PP00454; PI3 PI4 kinase; 1.
Pfam; PF00792; PI3K C2; 1.
Pfam; PF00794; PI3K_rbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB009636; BAA25634.1; -
                                    361 AATGGTTTGAAGGAA 375
                                                         AladiyLeuGlydiu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00239; C2; 2.
SMART; SM00142; PI3K C2; 1.
SMART; SM00144; PI3K rbd; 1.
SMART; SM00145; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PI3Kā; 1.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00613; PI3Ka
Pfam; PF00787; PX; 1
                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                       PK3G RAT
                                                                                                                                                                                                   PIK3C2G
                                                                                                                070173;
                                                                               RESULT 9
PK3G_RAT
ID PK3G
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490 AGGCATGTTTCCCCCCTTTTGGGTCCAGATGTCTTGTTAATCTTCTCCAAGGTACTTGGAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 TTCCCGGGGGGCACAGCTGTTTCCCATCATTTTGTGGGCCAGATGCCTCTGGCACTTCCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 CAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAGGTGGAGGGTGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 GlyGluAspProArgPheSerAlaLeuThrProSerSerThrGlyLeuAspLysCysHis 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 TCAAACCATTTTCTTCCTCTGCTGCTTCTTGGGCATGATCTTCGGGAAGATTCTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 GGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGTTTCGATCGT---TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lattard V., Longin-Sauvageon C., Lachuer J., Buronfosse T., Benoit E. "Cloning, sequencing and tissue dependent expression of FMO1 and FMO3 in the dog.";
in the dog."; Submitted (MAY-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: This protein is involved in the oxidative metabolism of a variety of xenobiotics such as drugs and pesticides.
-!- CATALYTIC ACTIVITY: N, N-dimethylaniline + NADPH + O(2) = N, N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dimethylaniline monooxygenase [N-oxide forming] 1 (BC 1.14.13.8)
(Hepatic flavin-containing monooxygenase 1) (FMO 1) (Dimethylaniline oxidase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 CCTIGAAACCTAGTTTAGTCATGACCTCATAGTTTAGCTTCATATACA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 GinginglyGinSerglyThrGluHisCysAsnTyrTyrVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1402 1499 C2 DOMAIN.
1505 AA; 170974 MW; 5ED4C2239968C4B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1505
33
16
50
17
5
| SMART; SM00312; PX; 1. | PALSE NEG. | PROSITE; PRO0499; C2 DOMAIN 1; FALSE NEG. | PROSITE; PS0004; C2 DOMAIN 2; FALSE NEG. | PROSITE; PS00016; PI3 4 KINASE 1; 1. | PROSITE; PS00016; PI3 4 KINASE 2; 1. | PROSITE; PS50290; PI3 4 KINASE 2; 1. | PROMAIN 976 1240 PI3K/PI4K. | PANASIN PIAK. | PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-975-856-1 (1-576) x PK3G_RAT (1-1505)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.95
89.50
42.24%
28.45%
8.89%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FMO1 CANFA
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protein 1).
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               565 ACTOGICATOTICCICAGGGICGCIGAICTOTICATAAACCACCAGCIGCITICICICAC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 GCAGTCTGTGGGTCCAGGCATGTTTCCCCCTTTTGGGTCCAGATGTCTTGTTAATCTTCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 CCAAGGIACTIGGATTICCCGGGGGGCACAGCTGTTICCCATCATTITGTGGGCCAGATG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 CCICTGGCACTICCITCAAACCATITICTICCICTGCTGGCTICTTGGGCATGATCTTCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 GGAAGAITCTCTGGAGGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ArgpheSerLeuLeuLysCysIl 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ITCGATCGTTACCAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PheProGluAspTyr 77
                                                                                                                                                                                          PRINTS; PRO0419; ADXEDTASE.
PRINTS; PR00368; FADPUR.
PRINTS; PR00370; FMOXYGENASE.
Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ------YalSerAsnSerCysLysGluMetSerCys----
                                                                                                                                                                                                                                                                                                                                                                                                                            ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                 FAD (ADP PART) (POTENTIAL)
NADP (POTENTIAL)
9F3458484540521F CRC64;
                                                                                                                                                                                                                                                                                                                      531
14
14
36
40
                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
dimethylaniline N-oxide + NADP(+) + H(2) O. COFACTOR: FAD (By similarity).
SUBCELLULAR LOCATION: Microsomal.
TISSUE SPECIFICITY: Liver.
                                                                                                                                                                                                                                   Transmembrane, Multigene family; Acetylation.
INIT MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 -----TyrSerAspPhePro-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743 AA.
                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                        SIMILARITY: Belongs to the FMO family.
                                                                                                                                                                                                                                                                                                                                                                                           US-09-975-856-1 (1-576) x FMO1_CANFA (1-531)
                                                                                                                                         EMBL; AF384053; AAK97433.1; -.
InterPro; IPR00159; Adrndx_reductase.
InterPro; IPR001327; PAD_pyr_redox.
InterPro; IPR000960; Flav cont_mnoxgn.
Pfam; PF00743; PMO-like; I.
                                                                                                                                                                                                                                                                 13 FA
195 NA
59927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _REP1 MOUSE STANDARD;
054916; Q8C9U9; Q99LR8;
10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                    0.996
88.50
38.21%
26.83%
8.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGGAG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 nirpdiu 125
                                                                                                                                                                                                                                                                  8
190
531 AA;
                                                                                                                                                                                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                              INIT MET
MOD RES
NP BIND
NP BIND
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                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            Query Match:
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REP1_MOUSE
ID REP1_MC
AC O54916;
DT 10-OCT-
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RA MEDILINE-ZAZJAGOSI, PUDMEGE-LIAGOSDI,
RA MEDILINE-ZAZJAGOSI, PUDMEGE-LIAGOSDI,
RA MAGARINE-ZAZJAGOSI, PUDMEGE-LIAGOSDI,
RA YAGIR K. TORMATO Y., RASUNKAM Y., NOGAMIA, Y., SCHORDACH C., GOJODORI T.,
RA YAGIR K., TORMATO Y., HASEGAWA Y., NOGAMIA, Y., QUACKERDHOSH J.,
RA BALGAREJII R., Hill D.P., Bult C., Hume D.A., Quackerbush J.,
RA BALGAREJI R., REAGID D., BRUSIC V., CHOCHIA C., CORDANI L.B., Cousins S.,
RA GARRET J., BRAGAL D., BRUSIC V., CHOCHIA C., CORDANI L.B., COUSINS S.,
RA GARRET R., REAGID J., RICKORN R., GOUGH J.,
RA GARRET R., KAWAJI H., KAWASBAWA Y., KEGAZIK R., GOUGH J.,
RA GARAIA A., KANCOKKIN I.V., LEC Y., LENHARG B.L.,
ROMAGASHAM T., WALCHONIN I.V., LENHARG B.L., MIKE B.L.,
RAGASHAMA T., NUMBATA K., OKIGO T., PAVAN W.J., PERTEA G., PESOLE G.,
RAGASHAMA T., NUMBATA K., OKIGO T., PAVAN W.J., PERTEA G., RINGWAL M.,
SANDGELIN A., SCHNEIGER C.A., SECTOU M., Shimada K.,
SANDGELIN A., SCHNEIGER C.A., SECTOU M., SHIMADA R.,
SULTANA R., TAXENAKA Y., TAYLOR M.S., TEAGGALE R.D., TOMITA M.,
SANDGELIN A., SCHNEIGER C.A., SECTOU M., SHIMADA R.,
NAGARAMA T., KANDA B.A., YANDG I., YANG I.,
WHIMING L.G., WYNSHAW-BORIS A., YANGAGAR R.D., TOMITA M.,
SALTAR R., SAKAN T., KAWAI J., AIZAWA R., SAKAZUME N., SALTOK N.,
RA HIROZANE-KIRIKAWA T., KOMIN H., NAKAMURA M., YANG I., FULVUGA S.,
RA MIYAZAKI A., SAKAI K., SASBAKI D., SAIDARAWA T., FULVUGA S.,
YANDISAKI T., RAYASHIZKH Y., ITOH M., YARAWA I.,
KANDARAKI T., RAYASHIZKH Y., ISHII Y., ITOH M., YAGARWA I.,
YABURISHI A., YOSHINO M., WATEFSTON R., ATARWA T., FULVUGA S.,
YABURISHI A., YOSHINO M., WATEFSTON R., ATARWA T., FULVUGA S.,
YABURISHI A., YOSHINO M., WATEFSTON R., LANGER B.S., ROGERS J.,
YABURISH S., HAYASHIZKH Y., TANDKA "., TA
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MEDINE-213825; PubMed=12477932;

MEDINE-213825; PubMed=12477932;

MIGHINE-213825; PubMed=12477932;

MIGHINE-213825; PubMed=12477932;

MIGHINE-213825; PubMed=12477932;

MIGHINE-213825; PubMed=12477932;

MIGHINE-12, Colling P.S., Magner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul G.M., Hong L., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., End L., Marusina K., Farmer A.M., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brands M., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Abrahas S.S., Morley M.C., Malek J.A., Gunarathe P.H., Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Willalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ablakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Ablakealey R.W., Touchman J.W., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. Handle, J.M., Madan A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. Handle, J.M., Madan A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. Handle, J.M., Madan A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. M. Marra M.A., Schein J.E., Jones C. M. Madan A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C. M. Madan A., Schein J.E., Jones C. M. Marra M.A., Schein J.E., Jones C. M. Marra M.A., Schein J.E., Jones C. M. 
42, Last sequence update)
42, Last annotation update)
Eps domain containing protein 1 (RalBP1-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98058900; PubMed=9395447;
Yamaguchi A., Urano I., Goi T., Feig L.A.;
"An eps homology (EH) domain protein that binds to the ral-GTPase
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 447-743 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 8-743 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 272:31230-31234(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNAs.";
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                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                        10-OCT-2003 (Rel. RalBP1 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target, RalBP1.
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US-09-975-856-1 (1-576) x REP1_MOUSE (1-743)
                                                                                                                                                                                                                                                                                                                                                                                                                                           488 -----488 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 oLeuThrGlyProGlyPro 147
                                                        11 TyrPheGlyArgSerGlnPhe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE OF 185-207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
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                                                                                                                                        190
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                                                                                                                                                                                                                                                           available;
--- TISSUE SPECIFICITY: Expressed in all tissues examined. The highest level expression was found in the kidney and testis.
---- PIM: EGF stimulates phosphorylation on Tyr-residues.
---- SIMILARITY: Contains 1 EH domain.
---- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
---- SIMILARITY: Sef. 3 sequence differs from that shown due to a
                                                                                                                                  GRB2. Binding to RALBP1 does not affect its Ral-binding activity. Forms a complex with the SH3 domains of CRK and GRB2 which may link it to am EGS-responsive tyrosine kinase.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00018; EF HAND; 1.
PROSITE; PS50031; EF; 1.
Calcium-binding; Coiled coil; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QWETFSERSSSQTLTQFDSNIAPADPDTAIVHPV ->
VSKTSLSLLEISLFTGRSFKQDRFTAGYLQYAHTP (in
         [4]
STRUCTURE BY NWR OF 227-318.
MEDLINE=21285759, PubMed=11389591;
MEM S., Cullis D.N., Feig L.A., Baleja J.D.;
"Solution structure of the Repsi EH domain and characterization of its binding to NPF target sequences.";
Biochemistry 40.6776-6785.(2001).
                                                                                               -!- FUNCTION: May coordinate the cellular actions of activated EGF receptors and Ral-GTPases.
                                                                                                                       SUBUNIT: Homodimer (Potential). Interacts with RALBP1, CRK and
                                                                                                                                                                                                                        Name=2;
IsoId=054916-2; Sequence=VSP_007956, VSP_007957;
Note=Due to intron retention. No experimental confirmation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Fild=vsr 007957.
/FIId=VSP 007957.
25510D11254CF4A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH RALBP1.
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244
149
169
169
 Proc. Natl. Acad. Sci. U.S.A. 99:16899~16903(2002).
                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EF-HAND (POTENTIAL).
PRO-RICH.
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Indels:
Gaps:
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Matches:
                                                                                                                                                                                                Name=1;
IsoId=O54916-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isoform 2)
/FTId=VSP
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EMBL, AK041967; BAC31117.1; ALT INIT.
EMBL, BC002256.1; ALT_FRAME
PIR, T09173; T09173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1F16; 18-JUL-01.
MGD; MGI:1196373; Repsl.
InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
                                                                                                                                                                                                                                                                                                                                                 frameshift in position 719.
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88.00
38.92%
23.95%
8.59%
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SMART; SM00027; EH; 1.
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Query Match:
DB:
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273
273
273
273
236
368
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CA BIND
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TACTICTCTAAGAAAGAGGGAAAAGAIGAAAICCTCGGAGAAAAICGTCTAIGIGIAI 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 AGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGAAGAAAATGGTTTGAAGGAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
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                                                                                                                                                                                                          19 IleAlaLeuLysLeuValAlaValAlaGlnSerGlyPheProLeuArgValGluSerIle 38
                                                                                                                                                                                                                                                                                                                     39 AsnThrValLysAspLeuProLeuProArgPheValAlaSerLysAsnGluGlnGluSer 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 ProProProGlyArgGlyGlnValLysLysGlyProGlySerHisAspAlaValGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 GTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGCCCCCCCGGGAAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90343821; PubMed=2383273; Guan S.H., Falick A.M., Cashman J.R.; Murterminus determination: FAD and NADP binding domain mapping of hog liver flavin-containing monooxygenase by tandem mass spectrometry."; Biochem. Biophys. Res. Commun. 170:937-943(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dimethylaniline monooxygenase [N-oxide forming] 1 (EC 1.14.13.8)
(Hepatic flavin-containing monooxygenase 1) (FMO 1) (Dimethylaniline oxidase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The flavin-containing monooxygenase expressed in pig liver: primary sequence, distribution, and evidence for a single gene."; Biochemistry 29:119-124(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
MEDLINE=90212556; PubMed=2322534;
Gasser R., Tynes R.E., Lawton M.P., Korsmeyer K.K., Ziegler D.M.,
Philpot R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGAAACATG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ProArgProSerAlaGluGlnGln-----
                                                                                                                                                                                                                                                                                                                                                                                                                     223 CGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGAAACCAC-
                                                                                                                                                                                                                                                                                ------AAGGTCACCCTCCCACCTTCATGCGTAGTAAA-
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                                                                                                                                        151 ATGAAGCTAAACTATGAGGTCATGACTAAACTAGGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-13 AND 184-201, AND ACETYLATION
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266

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385 CCTCTGGCACTTCCTTCAAACCATTTTCTTCCTCTGCTGGCTTCTTGGGCATGATCTTCG 326
                                                                                                                                                             265 TTCGATCGTTACCAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAG 206
                                                                                                                                                                                                                                                                                                                103 eGlnPheLysThrLysValCysSerValThrLysHisGluAspPheAsnThrThrGlyGl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUBBRICE FROM N.A. (ISOPORMS 2 AND 3).

TISSUB-Brain, and Lymph;

MEDINEL-2388257; PubMed=1247,932;

Strausberg R.D., Feingold E.A., Grouse D.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Blat N.K.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Blat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toonhiyuk S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1). Mao Y., Xie Y., Zhou Z., Zhao W., Zhao W., Wang Y., Wang Y., Wang Y., Chen X., Wu C.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           325 GGAAGATTCTCTGGAGGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096077; QBNDR7; QBWU62; Q9BXY9;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RalBP1 associated Eps domain containing protein 1 (RalBP1-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloccker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May coordinate the cellular actions of activated EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors and Ral-GTPases (By similarity).
-!- SUBUNIT: Homodimer (Potential). Interacts with RALBBI, CRK and GRB2. Binding to RALBBI does not affect its Ral-binding activity. Forms a complex with the SH3 domains of CRK and GRB2 which may link it to an EGF-responsive tyrosine kinase (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo Sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              744 AA.
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                                                                                                                                                                                                                                                                                                                                                                               205 GTGGGAG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 ACTCGTCATCTTCCTCAGGGTCGCTGATCTCTTCATAAACCACCAGCTGCTTTCTCTCAC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGTCTGTGGGGTCCAGGCATGTTTCCCCCTTTTTGGGTCCAGATGTCTTGTTAATCTTCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAGGTACTIGGATTICCCGGGGGGCACAGCIGITICCCCAICATITIGIGGGCCAGAIG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem. Res. Toxicol. 11:1145-1153(1998).
-!- FUNCTION: This protein is involved in the oxidative metabolism of a variety of xemobiotics such as drugs and pesticides.
-!- CATALYTIC ACTIVITY: N,N-dimethylaniline + NADPH + O(2) = N,N-dimethylaniline + NADPH + O(2) = N,N-dimethylaniline N-oxide + NADP(+) + H(2)O.
                                                                                          of
                                                  Wu R.-F., Ichikawa Y.; A. A. essential 1979. In the substrate-binding site porcine FAD-containing monocaygenase."; Eur. J. Biochem. 229:749-753 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HIGH MANNOSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00159; Adrndx reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; PR00180; FAD_pyr_redox.
InterPro; PR001419; ADXRDTASE.
PRINTS; PR00340; ADXRDTASE.
PRINTS; PR00370; FMOXYGENASE.
Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome; Transmembrane; Multigene family; Acetylation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ValSerAsnSerCysLysGluMetSerCys----
                                                                                                                                                                                                                                                                                                                                 "N-glycosylation of pig flavin-containing monocxygenase form 1: determination of the site of protein modification by mass spectrometry." Toxicol. 11:1145-1153 (1998).
                                                                                                                                                                                                                                             MEDLINE=98451545; PubMed=9778310;
Korsmeyer K.K., Guan S., Yang Z.C., Falick A.M., Ziegler D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAD (ADP PART) (POTENTIAL).
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Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Microsomal.
-!- TISSUE SPECIFICITY: Liver.
-!- SIMILARITY: Belongs to the FMO family.
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                          MEDLINE=95278229; PubMed=7758472;
Wu R.-F., Ichikawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TyrProAspPhePro---
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                                                                                                                                                                                                                                                                                                         Cashman J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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SMART; SM00398; HMG; 1.
PROSITE; PS50118; HMG; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DNA BIND 49 117 HMG BOX.
                                                                                                                                                                                                                                                                                 451 ATTAACAAGACATCTGGACCCAAAAGGGGGAAACATG----
                                                                                                                            ::: |||:::
97 ValGlnProArgThrSerAlaAspAlaGln-----
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01-FRE-1996 (Rel. 31, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Transcription factor SOX-11.
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POLY-ALA.
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PIR; 150707; 150707.
HSSP; P44836; 1589
InterPro; IPR000910; HMG_12_box.
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    283 GAACGICCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_007954.
Missing (In isoform 3).
MISTID=VSP_007955.
A -> V (IN REF. 1).
V -> I (IN REF. 3).
SH -> FP (IN REF. 3).
W, IDFF2971IDB2BBE4 GRC64;
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                                                                                                             PTM: BGF stimulates phosphorylation on Tyr-residues (By similarity).
                                                                                                                                                       -!- SIMILARITÝ: Contains 1 EH domain.
-!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                   Name=2;
IsoId=Q96D71-2; Sequence=VSP_007953, VSP_007954;
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Missing (in isoform 2).
'mm7a-VSP_007954.
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Matches:
Conservative:
Mismatches:
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                                                                                          IsoId=Q96D71-3; Sequence=VSP 007955;
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isoId=Q96D71-1; Sequence=Displayed;
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EMBL; BC012764; AAH12764.1; -.
EMBL; BC021211; AAH21211.1; -.
EMBL; AL631900; CAD38569.1; -.
Genew; HGWC:15578; REPS1.
InterPro; IPR002048; EF-hand.
InterPro; IPR002061; EPS15_homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS00018; EF HAND; 1.
PROSITE; PS50031; EH; 1.
Calcium-binding; Coiled coil;
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SMART; SM00027; EH; 1.
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Best Local Similarity:
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                                  391 GGCCCACAAAATGATGGGAAACAGCTGTGCCCCCGGGAAATCCAAGTACCTTGGAAAG 450
                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGG 492
                                                                                                                                                                     -----GluProAla 109
                                                                                                                                                                                                                                                                                                                             110 SerProValValSerProGlnGln---SerProProThrSerProHisThr-TrpArgLy 128
---AspThr 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Embryonic expression of the chicken Sox2, Sox3 and Sox11 genes suggests an interactive role in neuronal development."; mech. Dev. 49:23-36(1995).
-!- FUNCTION: May function as switches in neuronal development.
-!- SUBCELULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Low level expression is seen in undifferentiated proliferating calls of neural epithelium. A greater expression is seen in the maturing neurons after they leave the neural epithelium. It is also found in the gut epithelium and adrenal medulla.
-!- SIMILARITY: Contains 1 HMG box domain.
79 ProProProGlyArgGlyGlnValLysLysGlySerValSerHis---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE=95267693; PubMed=7748786;
Uwanogho D., Rex M., Cartwright E.J., Pearl G., Healy C., Scotting P.J., Sharpe P.T.;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lania L.;
   GATATTGCCAAATACTTCTCTAAGAAAGAGTGGGAA 114
                                                                                                                                                                                                                                                                               -- Prophelle Arg Glu Ala Glu Arg Leu Arg 106
                                                                                                                                                                                                                                                                                                    ---AAACGGGCTGCAGACTTCCACGGAATGATTTTGGTAACGATCGAAACCACAGGAAT 276
                                                                                                                                                                                                                                                                                                                          ---ProAspTyrLysTyrArg--- 119
                                                                                                                                                                                                                                                                                                                                             277 CAGGITGAACGICCICAGAIGACIITICGGCAGCCICCAGAGAAICITCCCGAAGAICAIG 336
                                                                                                                                                                                                                                                                                                                                                                                       337 CCCAAGAAGCCAGCAGAAGAAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCA, 396
                                                                                                                                                                                                                                                                                                                                                                                                          124 ProLysMetAspProSerAlaLysProAsnAlaGlyGlnSerProGluLysAsnAlaPro 143
                                                                                                                                                                                                                                                                                                                                                                                                                                397 CAAAATGAGGAAACAGCTGTGCCCCCGGGAAATCCAAGTACCTTGGAGAAGATAAC 456
                                                                                                                                                                                                               115 AAGATGAAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATG 174
                                                                                                                                                                                                                                                                                                                                                                   ---ProArgLysLys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 GlyGlyGlySerLysSerAlaLysSerSerGlyLysLysCysSerLysLeuLysAlaAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 AlaAlaSerProProLysProGlyAlaLysAlaAlaProHisGlyAspTyrAlaGlyAsp 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -AGACTGCGTGAGAGAAGCAGCTGGTGGTTTAT 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 GluTyrValPheGlyAlaLeuLysValSerSerLysAlaValLysCysValPheValAsp 203
                                                                                                                                         :::|||||||
LysArgProMetAsnalaPheMetValTrpSerLys1leGluArgArgLys1leMetGlu 69
                                                                                                                           25 AGGAGACCCAGGGATGATGCTCAAATATCAGAGAGTTA-----CGAAAGGCCTTCGAT 78
                                                                                                                                                                                 175 ACTAAACTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN38 HUMAN STANDARD; PRT; 446 AA.
P17036; P13683; Q9NKNB; Q9NKJ1; Q9UC15; Q9UC16;
O1-APR-1990 (Rel. 14, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
zinc finger protein 38 (Zinc finger protein KOX25) (Zinc finger protein HF.12) (Zinc finger protein 3) (HZF3.1 protein).
ZNF38 OR KOX25 OR ZNF3.
 8E4B0A457F8BA833 CRC64;
                                396
45
22
67
77
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                                        Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 GluGluGluGluAspGluGluAspGluAspGlu 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGAGATCAGCGACCCTGAGGAAGATGACGAG 564
                                                                         Indels:
                                                                                                        (1-396)
                                                                                                                                                                                                                                    MetLeuLysAspSerGluLysIle----
                                                                                                                                                                                                                                                                                                                       107 LeuLysHisMetAlaAspTyr--
                                                                                                      US-09-975-856-1 (1-576) x SX11_CHICK
43503 MW;
                             1.49
86.50
31.75%
21.33%
8.44%
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TISSUE=Ovary, and Skin;
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396 AA;
                                                  Percent Similarity:
Best Local Similarity:
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                     Alignment Scores:
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
Altausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausherg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
A Stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenertion and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-!- FUNCTION: INVOLVED IN CELL DIFFERENTATION AND/OR PROLIFERATION.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pannuti A., Lanfrancone L., Pascucci A., Pelicci P.G., la Mantia G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thiesen H.-J.; "Multiple genes encoding zinc finger domains are expressed in human cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosati M., Marino M., Franze A., Tramontano A., Grimaldi G., "Members of the zinc finger protein gene family sharing a conserved N-terminal module.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Colon mucosa;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., 180gai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; BC013603; AAH13603.1; ALT_INIT.
EMBL; X60123; CAB4195.1; -
EMBL; AX000223; BAA91019.1; -
EMBL; X52356; CAA35582.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91145339; PubMed=2288909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 252-446 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-250 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-387 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Biol. 2:363-374(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FINGER PROTEINS
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us-09-975-856-1.rsp

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90 LeuAspArgGluThrArgThrGluAsnAspGlnGluIleSerGluAspThrArgSerHis 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 GTCTATGTGTATATGAAGCTA---AACTATGAGGTCATGACTAAACTAGGTTTCAAGGTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 ACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGGACTTCCACGGGAATGATTTTTGGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AATCAGGTTGAACGTCCTCAGATGACTTTC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 GATATTGCCAAATACTTCTCTAAGAAGAGTGGGAAAAGATGAAATCCTCGGAGAAAATC 138
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                         L -> P (IN REF. 2).

GEKPY -> IRDSG (IN REF. 5).

GEKPYGENEGGRAFESGENHYGHORIHTGEKPYECMEGGK

FGYSSGLIGHQ -> EALPTFVTLIRLLESVDPIVTNEAAF

PASSLATIPALIMELFCHHSLMFKKV (IN REF. 3).

67A6926807304782 CRC64;
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442
23
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::|||
| LeuTyrArgAspValMetLeuGluAsnTyr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-975-856-1 (1-576) x ZN38_HUMAN (1-446)
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EMBL; X07290; CAA30269.1;
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Best Local Similarity:
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33244
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138
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                                 349 GCAGAGGAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGG 408
                                                                                                      409 AAACAGCTGTGCCCCCCCCGGGAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGA 468
                                                                                                                                                                          469 CCCAAAAGGGGGAAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGTT
                                                                                                                            -----ProLeuGlyAsn---SerProGlyGluArgLeuAsnArg----
                                                                                                                                                                                                                                               529 TATGAAGAGATCAGCGACCCTGAGGAAGATGACGAG 564
                                                                                                                                                                                                                                                                                 161 GludluLysLeuThrProArgGlyGluArgSerGlu 172
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Search completed: March 31, 2004, 13:58:04 Job time : 18 secs

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Sequence:

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homo homo

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Q002t4 muss musculu Q0523 mus musculu Q0523 mus musculu Q05201 homo sapien Q01230 homo sapien Q01230 homo sapien Q01230 homo sapien Q01230 homo sapien Q01250 homo sapien Q01230 homo sapien Q01230 homo sapien Q01250 homo sapien
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Q8twh2 methanosarc
Q8twn7 methanosarc
Q8tma0 methanosarc
Q8tl12 methanosarc
Q8tl12 methanosarc
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
GO:0002818; AH02818.1.
GO:0005622; C:intracellular; IEA.
GO; GO:0006355; F:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003655; KRAB.
InterPro; IPR003655; KRAB.
FIGHT; SM00349; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                     096qil | 096qi0 | 099444 | 08wwz9 | 09nzk4 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JOCT-2003 (TrEMBLrel. 25, Last amotation update)
Similar to synovial sarcoma, X breakpoint 2.
Homo sapiens (Human)
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Q9BRW7
Q96QI0
Q96QI0
Q9Y444
QBWWZ9
Q9NZK4
Q8OZZ4
Q8C5Z3
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Q80TC5
Q8BVH0
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Q8TTY7
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Q86TD5
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Q8N2J5
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TISSUE=Placenta;
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   09BU88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9bu88 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                  ATGAACGGAGACGACGTT.....ATGACGAGTAACTCCCCTCG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                         using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                              BLOSUM62
Xgapop 10.0, Xgapext (
Ygapop 10.0, Ygapext (
Fgapop 6.0, Fgapext (
Delop 6.0, Delext
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_bacteriap:*
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seq length: 200000000
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sp_virus:*
                                                                                                                                                                   US-09-975-856-1
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Match Length DB
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                                                                        protein search,
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Database :

No. Result

Minimum DB Maximum DB

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Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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78.21%
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                  SEQUENCE FROM N.A. TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Pred. No.:
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ProProGlyLysProThrThrSerGluLysIleHisGluArgSerGlyAsnArgGluAla 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ThrHisAsnArgAspPro-Ly8GlyGlyAsnMetProGlyProThrAspCy8ValArgGl 220
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                                                                                                                                                                                                                                                                                                                                                               121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
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2BF8E1FFA4D58094 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Synovial sarcoma, X breakpoint 3.
                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                   x Q9BU88 (1-223)
PS50806; KRAB_RELATED;
                    25173 MW;
                                                                                 1.15e-62
685.50
66.07%
61.16%
66.88%
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                      223 AA;
                                                                                                                                                                                                                                     US-09-975-856-1 (1-576)
                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                            Alignment Scores:
Pred. No.:
PROSITE;
SEQUENCE
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DB:
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Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
GO: 00005904; AR405904.
GO: 00005625; P: ategalation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001909; KRAB_related.
InterPro; IPR003655; KRAB_related.
Ffam; PF01352; KRAB; 1.
SMART; SM00349; KRAB; 1.
SMART; SM00349; KRAB; 1.
SEQUENCE 170 AA; 19457 MM; D98IF807A9C7EABI CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ54B20.1.1 (Novel SSX family protein (Isoform 1)) (Fragment).
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EMBL; Z98304; CAC41947.1;
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Grafham D.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 2983-04; CAC41946.1; --
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005652; C:intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001999; RRAB.
InterPro; IPR001999; RRAB.
InterPro; IPR001999; RRAB.
Pfam; PF01352; KRAB; I.
SWART; SM00349; KRAB; I.
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Mammalia, Eutheria, Primates, Cararrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-007-2003 (TrEMBLrel. 25, Last annotation update)
DJ54B20.1.2 (Novel SSX family protein (Isoform 2)) (Fragment)
DJ54B20.1.2
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                         06EC7C89D35A1A30 CRC64,
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Matches:
Conservative:
Mismatches:
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Gaps:
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 25, Last ann
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576.00
80.65%
72.90%
56.20%
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Best Local Similarity:
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0003575; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001909; KRAB.
InterPro; IPR001855; KRAB.
PF01352; KRAB; I.
SMO0349; KRAB; I.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SYT-SSX protein (Fragment).
SYT-SSX protein (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
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                                                                                                              PROSITE, PS50806; KRAB RELATED; 1.
NON TER 196 196
SEQÜENCE 196 AA: 22200 No.
                                                                                                                                                                                                                                       4.59e-48
545.50
63.78%
57.65%
53.22%
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Best Local Similarity:
Query Match:
DB:
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Length:
Matches:
Conservative:
Mismatches:
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          US-09-975-856-1 (1-576) x Q8WWZ9 (1-64)
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247.50
50.88%
45.61%
24.15%
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Clark J., Rocques P.J., Crew A.J., Gill S., Shipley J., Chan A.M.,
Gusterson B.A., Cooper C.S.;
"Identification of a novel genes, SYT and SSX, involved in the t(X;18)
(p11.2;q11.2) translocation found in human synovial sarcoma.";
NAt. Genet. 7:502-508(1994).
EMBL: X79200; CRB36970.1; -.
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Interpretation of the total series of th
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Sukaryota: Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
BA564H18-1 (Synovial sarcoma, X breakpoint 2) (Fragment).
SSX2.
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                                           SEQUENCE FROM N.A.
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                                     GluArgFroGlnMetThrPheGlyArgLeuGlnGlyIleSerProLysIleMetProLys
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SEQUENCE FROM N.A.
MEDLINE=20210694; PubMed=10749136;
dos Santos N.R., Torensma R., de Vries T.J., Schreurs M.W.J.,
dos Santos N.R., Torensma R., de Vries T.J., Adema G.J.,
de Bruijn D.R.H., Kater-Baats E., Ruiter D.J., Adema G.J.,
van Muijen G.N.P., Geurts van Kessel A.;
"Heterogeneous expression of the SSX cancer/testis antigens in human
melanoma lesions and cell lines.";
Cancer Res. 60:1654-1662(2000).
EMBL, AF190791; AAF44724.1; -.
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41 IleHimGluArgSerGlyAmnArgGluAlaGlnGluLymGluArgArgGlyThrAla
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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"Analysis of the mouse transcriptome based on functional annotation of
"C,770 [full-length CONSS.";
"Analysis of the mouse transcriptome based on functional annotation of
"C,770 [full-length CONS.";
"A Nature 420:563-573 (2002).
"B EMBL; AK076879; BAC36519.1; -..
"B GO; GO:0005672; C:intracellular; IEA.
"GO; GO:0005672; F:mucleic acid binding; IEA.
"B GO; GO:0005672; F:mucleic acid binding; IEA.
"R FRO:1572; RRAB; 1.
"R PROSITE; PS50806; KRAB; 1.
"R PROSITE; PS50806; KRAB; 1.
"R PROSITE; PS50806; KRAB RELATED; 1.
"M Hypothetical protein.
"SEQUENCE 165 AA; 19584 MW; 5FE61134DDB7BAC4 CRC64;
                                                                                                       ArgGluArgLysTyrArgVallleTyrGluGluIleSerAspProGluGluGluGluAsp
                                                                      CGTGAGAGAAAGCAGCTGGTGTTTATGAAGAGATCAGCGACCCTGAGGAAGATGACGAG
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                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical KRAB box/KRAB-related containing protein.
Mus musculus (Mouse).
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TYBAIN-ESTBL/67, TISSUE-Testis;
MEDIINE-22354683; PubMed-12466851;
The FANTOM COMBOTTIUM:
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Q8C5Z3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: ||||||||| :::||||||| SerThrTyrPheSerAspGluGluIrpGlyLysLeuThrGlnTrpGlnLysSerAlaTyr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 CCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 AACCACAGGAATCAGGITGAACGICCTCAGAIGACTITCGGCAGCCICCAGAGAATCITC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 GAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGAAACATGCCTGGACCCCACAGACTG 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transberg R.;
Strausberg R.;
Submitted (MAR.2003) to the EMBL/GenBank/DDBJ databases.
BrBL; BCO48441; AFH4841.1; -..
BR GO:0005622; C:Intracellular; IEA.
BR GO:0005676; F:mucleic acid binding; IEA.
BR GO; GO:00053676; F:mucleic acid binding; IEA.
BR HIGERFO: IPRO01809; KRAB.
BR HIGERFO: IPRO01809; KRAB.
BR PFam; PFO1352; KRAB. 1.
BR PROSITE; PSSO806; KRAB; 1.
BR PROSITE; PSSO806; KRAB, 1.
BR PROSITE; PSSO806; KRAB, 1.
SCUENCE 128 AA; 15290 WW; F88614DICBFF3B70 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AGGAGACCCAGGGATGATGCTCAAATATCAGAGAAGTTACGAAAGGCCTTCGATGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAAATACTTCTCTAAGAAAGAGTGGGAAAAGATGAAATCCTCGGAGAAAATCGTCTAT
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                                                                                                                                                                                             01-JUN-2003 (TrENBLrel. 24, Created)
01-JUN-2003 (TrENBLrel. 24, Last sequence update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
51milar to RIKEN cDNA 4930414C09 gene.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Rodentia; Sciurognathi, Muridae, Musinae; MusCBI_TaxID=10090;
                      523
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56
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36
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                                        CATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGG
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Matches:
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                                                                                                                                                               PRT;
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214.50
45.00%
31.11%
20.93%
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Percent Similarity:
Pest Local Similarity:
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US-09-975-856-1 (1-576) x Q9CPU1 (1-170) Qy 67 AAGGCCTTCCATGATATTGCCAAATACTTCTCTAAGAAAGA	23 GAGGARATGATTTGGTAAGGATGAACACGAAGGAAGGAAGGAAGGA
Db 121	997UT 10 997UT

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Alignment Scores:
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                                                                             88 GluGlyAsnAspSerdluGluValProGluAlaSerGlyProGlnAsnAspGlyLysGlu 107
                                                                  GAAGAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCCACAAAATGATGGGAAACAG 414
                     295 ATGACTITCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 ITCCCGAAGAICAIGCCCAAGAAGCCAGCAGGAAGAAAAIGGIITGAAGGAAGIGCCA 381
                                              87
53 GlyGlnGlnTyrGlyGlyTyrArgProThrGlnProGlyProProGlnProProGlnGln 72
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----TyrAspGlnIleMetProLysLysProAlaGlu
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Y.,
Nilsson G., Larsson O.;
Submitted (Aug.-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AY138488; AAN39530.1; -.
NON TER 39 39
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Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Nilsson G., Larsson O.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               8FC179F66C8C7E0D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GluAlaSerGlyProGlnAsnAspGlyLysGluLeuCys 39
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SS18/SSX2 fusion protein (Fragment).
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Matches:
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Mismatches:
Indels:
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4336 MW;
                                                                                                            CTGTGCCCCCGGGA 429
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137.00
87.88%
75.76%
13.37%
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                                           73 ArgProTyrdly
                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                              39 AA;
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                355
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322 ITCCCGAAGAICAIGCCCAAGAAGCCAGCAGAAGAAAAIGGIITGAAGGAAGIGCCA 381
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Nilsson G., Larsson G.,
                                                                                                     8FC179F66C8C7E0D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SS18/SSXZ fusion protein (Fragment).
SS18/SSXZ Fusion protein (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SS18/SSX2 fusion protein (Fragment).
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Matches:
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Matches:
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                                                                                                                                                                                 1.51e-05
137.00
87.88%
75.76%
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4336 MW;
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137.00
87.88%
75.76%
EMBL, AY138489; AAN39531.1;

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NON TER 3 3

SEQÜENCE 39 AA, 4336 MW;
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                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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| Second | S
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Search completed: March 31, 2004, 13:59:50 Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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March 31, 2004, 15:16:19; Search time 2745 Seconds (without alignments) 6266.162 Million cell updates/sec US-09-975-856-1 Perfect score: Run on: Title:

1 ATGAACGGAGACGCCTT......ATGACGAGTAACTCCCCTCG 576 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST: * Database

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em gss hum: *
em gss inv: *
em gss pln: * em_esthum: *
em_estin: *
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em_estpl: *
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em_hts: *
gb_est1: *
gb_est3: *
gb_est3: *
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em_gss_vrt:* em_gss_fun:* em_gss_mam:* em_gss_phg:* em_gss_vrl:* gb_gssl:* gb_gss2:* em_gss_pro:* em_gss_rod:* em_gss_mus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			uo.	111111111111111111111111111111111111111	BM806411 AGENCOITET	THENCOMED .	RITHELT AGENCOLIRT	3Q222907 AGENCOURT	
			Description		BM806411	BIII 94624	BIT161779	BQ222907	
SUMMARIES			ID		BM806411	BU194624	BU161779	13 BQ222907	
			DB	1 1	12	13	13	13	
			Match Length DB		979	836 13	887	863	
	dю	Query	Match		86.2	85.9	85.9	85.2	
			Score	1	496.6	495	495	491	
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BM471266 BQ434972 BU170242 BQ432374	BE535379 CB158955 BQ231752 B1560469 BO229996	BE408883 BE891434 CD767542 BE410950	BQ229064 BQ333981 BE408978 CB156144 BE384545	BG4/8295 BE390290 BF211114 BG104299 BQ224117 BB387586 BU189304	602 1126 1987 1697 1936 217	BE896093 BE866727 BUL78938 AA312651 BF212335 CB143725
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ALIGNMENTS

ISM Homo sapiens

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 979)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies of Contact Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LiAM12288 row: f column: 11

High quality sequence stop: 622. AGENCOURT 6542819 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548810 5', mRNA sequence.
BM806411.1 GI:19123234
EST. Homo sapiens (human) ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 1 BM806411

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254 ciradeirircaadeccaccereceaecriricarereraraaraaaegeeegaadacriecag 313
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
(LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.f column: 16
Plate: LLAM13525 row: f column: 16
High quality sequence stop: 624.
Location/Qualifiers
1. 836
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 85.9%; Score 495; DB 13; Local Similarity 91.3%; Pred. No. 4.9e-131; es 525; Conservative 0; Mismatches 5C;
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  AUTHORS
TITLE
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AGENCOURT_7969283 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6165903
                                                                                                                /tissue_type="melanotic melanoma"
/tab host="DH1DB (phage-resistant)"
/clone_lib="NHH MGC_72"
/note="Organ: skin, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 836)
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Pred. No. 1.8e-131;
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                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                    organism="Homo sapiens"
                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5548810"
Location/Qualifiers
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SOURCE
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AGENCOURT_7675894 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6095680 BQ222907
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435 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGAAAAAAGAGCTGTGC 494
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/lab host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Moverage insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 863)

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Context: Robert Strausberg, Ph.D.

Email: ggapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Conscrtium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

http://image.llnl.gov

Plate: LLAM1368 row: h column: 17

High quality sequence stop: 625.
                                                             CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                   cccceegaaaaccaacraccrcreagaagarrcaceagagarcregacccaaaagggg
                                                                                                                                                                                481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAGCAGCTGGTGGTTTTATGAAGAGATC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                       541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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91.2%; Pred. No. 7e-130;
iive 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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                                                                   887 bp mRNA linear BST 04-SEP-2002
.7858401 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6168477
                                                                                                                                                                                                                                                                                                                                                                                                                                                               L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: ArcCoCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1353 z row: a column: 22
High quality sequence stop: 739.
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/clone lib="with MGC 7"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: Not1;
/note="organ: skin; Vector: pCMV-SPORT6; Site 1: Not1; Vector: pCMV-SPORT6; Site 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGCCTCAGAAAATCTTCTATGTGTATATGAAGAGAAGTATGAGGCTATGACTAAA 254
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                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.1e-131;
0; Mismatches 50;
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/clone="IMAGE:6168477"
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Best Local Similarity 91.3%;
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                      521; Conservative
       Local Similarity
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/db_xref="taxon:9606"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT 6478381 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5563101
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                                                                                                                   364
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1 (Dases 1 to 1001)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                     ATGATTTTGGTAACGATCGAAACCACGGAATCAGGTTGAACGTCCTCAGATGACTTTCG
                                                                           241 ATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACTTTTCG
                                                                                                                                                                GTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAAACAGCTGTGCCCCC
                                                                                                                                                                                              ATTCGGAGGAAGTGCCAGAAGCATCTGGCCCCACAAATGATGGGAAAGAGCTGTGCCCCC
                                                                                                                                                                                                                         CGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGAAAC
                                                                                                                                                                                                                                             ATGCCTGGACCCACAGACTGCGTGAAAAACAGCTGGTGATTTATGAAGAGATCAGCG
GTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGGCTGCAGACTTCCACGGGA
                                                                                                             GCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGAAGAAAATG
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LIAMI2293 row. i column: 22
High quality sequence start: 258
High quality sequence stop: 436.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       ACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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AUTHORS
TITLE
JOURNAL
COMMENT
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Length 1001;

DB 12;

84.8%; Score 488.6;

Query Match

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Homo sapiens cDNA clone IMAGE:6159943
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation. Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Link.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAM13509 row: n column: 08
High quality sequence stop: 634.
Location/Qualifiers
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  Pred, No. 3.7e
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AGENCOURT 7896851 NIH_MGC_72
5', mRNA Sequence.
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/mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6159943"

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_7844770 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6051106
/tissue_type="melanotic melanoma"
/lab host="PHIOB (phage-resistant)"
/clome lib="NHI MGC 72"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Ingent Skin; Vector: pCMV-SPORT6; Site_1: NotI;
/rester insert size 2 kb. Library constructed by Life Technologies."
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1 (bases 1 to 873)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                    Score 481.6; DB 13;
Pred. No. 3.4e-127;
0; Mismatches 59;
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               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: LLAM13304 row: g column: 11
High quality Sequence stop: 696.
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/tote="Caracter and antidirectionally."
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1. .1135
| / organism="Homo sapiens" |
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| mol_type="mRNA" |
| db_xref="taxon:9606" |
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| / oll line="MGC36" |
| / lab_host="MB108" |
| / clone=lib="NHH MGC 10" |
| / note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
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601058532F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445470 5',
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Contact: Robert Strausberg, Ph.D.
Email: gapbs-remail.nih.gov
Tissue Procurement: Arc.
CDNA Library Preparation: Life Technologies, Inc.
CLOS Genencing Princyte Genomics, Inc.
Close distribution: MGC close distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8415 row: o column: 07
High quality sequence stop: 650.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1135)
NIH-MGC http://mgc.nci.nih.gov/
National Instituce of Health, Mammalian Gene Collection (MGC)
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               CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCCAAAAGGGGG
                                                                                                  AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTTATGAAGAGATC
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 10 8568 i Lo 888)

National Institutes of Health, Mammalian Gene Collection (MGC)

Interpolate: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be thtp://image.llni.gov

Plate: LLAMM3530 row: j column: 22

High quality sequence stop: 636.

Location/Qualifiers
                        BQ432374

BQ432374

AGENCOURT_7859139 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6167925
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/lab_host="hH10B (phage-resistant)"
/clone_lib="NHH MGC_72"
/note="forgan: skin; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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llarity 89.8%; Pred. No. 3.6e-127;
Conservative 0; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="mRNA"
db_xref="taxon:9606"
                                                                                   BQ432374
BQ432374.1 GI:21171450
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K-EST0218399 L18POOLIN1 Homo sapiens CDNA clone L18POOLIN1-32-F07
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Kim, N.S., Bahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                      GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yusseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
Fax: +82-42-860-c409
Fax: +92-2-80-0-409
Fax: +92-2-80-0-409
Fax: +92-2-80-0-409
Fax: +92-42-860-602
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Unpublished (2002)
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Score 471.6; DB 14; Length 602; Pred. No. 2.2e-124;

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC/COTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13343 row: i column: 08
High quality sequence stop: 532.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this
                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shirah
Toshlyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.lih.gov
Plate: LiAM.1751 row: e column: 09
High quality sequence stop: 790.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 GAAAGCCTCGGAGAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTAGGTTTCAAGGCCACCCTCCCACCTTTCATGTAATAAACGGGCCGAAGACTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CGGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCTCAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCGGCAGGCTCCAGGGAATCTCCCCGAAGATCATGCCCCAAGAAGCCAGCAGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 CCCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGATCTGGACCCAAAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAA-GAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622 GGAACATGCCTGGACCCCCAGACTGCGTGAGAAAAAAAGGCTGGTGATTTATGAACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.9%; Score 454.6; DB 12; 90.1%; Pred. No. 2e-119; cive 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539 TCAGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
                                                                                                                                                                                                                                                                                                             sapiens"
                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5296880"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arccadadecriceardararreccadararrecricidadeagagagagadagare 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAGGGGG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGCCTCAGAGAAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chadentroaadeccaccereceaecrireardraraaagegggeggagaerrecag 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAATGACGTGGATAATGACCCTAACCGTGGAATCAGGTTGAACGTCCTCAGATGACT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAATGATGGGAAAGAGCTGTGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccceseanarcchactrecretenenaritenesagarctesagacccananases
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6066127"
/tissue_type="melanotic melanoma"
/lab host="HHIOB (phage-resistant)"
/lab host="NHHOB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dr
Average insert size 2 kb. Library constructed by Life
Technologies."
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11 (Dases 1 to 793)
11 MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                         1 ATGAACGGAGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAAG
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                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                             Length 950;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                           Score 470.8; DB 13;
Pred. No. 4.8e-124;
0; Mismatches 57;
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89.9%;
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BI560469.1
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Best Local Simil
Matches 516; C
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SOURCE
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BE408883 573 bp mRNA linear EST 21-JUL-2000 601303758F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637982 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab bost="Diplomerations"
/clone_lib="NIH MGC_21"
/clone_lib="NIH MGC_21"
/note="Corpan: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by Oilgo-dT priming.
Directionally cloned into ECORIXAnoI sites using the
following 5' adaptor: GGGACGAG(G). Size-selected >500bp
for average insert size_1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                463
                                                                                                                                                                                            538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   524 GAAACAIGCCIGGACCCACAGACIGCGIGAAAGAAAGCAGCIGGGGATITIAIGAAGAGA 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 573)

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                                                                480 GAAACAIGCCIGGACCCACAGACIGGGGGAGAAAGCAGCIGGIGG-TITAIGAAGAGA
                                     361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGGAAACAGCTGTGC
                                                                                                                CCCCCGGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAA-GGGG
                                                                                                                                               464 CCCCCAGGAAAAGCAAATAATTCTGAGAATTAATAAGAGAGATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 573)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                     576
                                                                                                                                                                                                                                                             539 TCAG-CGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
                                                                                                                                                                                                                                                                                         TCAGCCGACCCTGAGGAAGATGACGAGTAACTCCCCTGG
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Pred. No. 1.2e-110;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE408883.1 GI:9345333
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88.9%;
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Matches 458; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                                                   584
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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_7560406 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6048424
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NIH-MGC http://mgc.nci.nih.gov/.
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/lab_host="DHIOB (phage-resistant)"
/clone lib="NHH MGC 72"
/note="Organ: skin, Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, Primer: Oligo dI
Average insert size 2 kb. Library constructed by Life
Technologies.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13297 row: g column: 17
High quality sequence stop: 483.
Location/Qualifiers
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682 TCAGGGACCTGAGGAAAGATGACGAGTAACTCCCCTC 718
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Pred. No. 3.3e-117;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                            BQ229996.1 GI:20411396
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89.1%;
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                                                                                                                                                     mRNA sequence.
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AGENCOURT
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TITLE
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BQ229996
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867 bp mRNA linear EST 20-OCT-2000
601434893P1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919991 5',
418
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/mol_type="mixth" bagtens

/db_xref="taxon:9606"

/clone="lmAGE:3919991"

/tissue_type="melanotic melanoma"

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/clone lib="NIH MGC 72"

/clone lib="NIH MGC 72"

/clone lib="NIH MGC 72"

/clone lib="XII Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."
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1 (bases 1 to 80; no. 1 nib; gov/.

NIH-MGC http://mgc.no; nib; gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAAACTATGAGGTCATGACTAAA
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Tissue Procurement: ATCC/DCTD/DTP
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9750 row: j column: 24
High quality sequence stop: 641.
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/organism="Homo sapiens"
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TITLE
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KEYWORDS
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                                          5;
           Length 867;
                                          Indels
           DB 10;
     Score 423.4; DB 10;
Pred. No. 1.9e-110;
0; Mismatches 56;
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   73.5%;
Query Match
Best Local Similarity 89.4
Matches 512; Conservative
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